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PATENT

Customer No. 22,852

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Brigitte GICQUEL et al.

Application No.: 09/855,604

Filed: May 16, 2001

For: POLYPEPTIDE NUCLEIC
SEQUENCES EXPORTED FROM
MYCOBACTERIA, VECTORS
COMPRISING SAME AND USES
FOR DIAGNOSING AND
PREVENTING TUBERCULOSIS

Group Art Unit: 1635

Examiner: Unassigned

Commissioner for Patents
Washington, DC 20231

Sir:

REQUEST FOR APPROVAL OF DRAWING CHANGE

Subject to the approval of the Examiner, it is respectfully requested that Figs. 1-57B (185 sheets) in the above-captioned application be amended as shown in the attached marked-up drawings. The changes are marked-up on the attached copies of the original filed drawings.

Applicants will submit formal versions of the revised drawings in due course upon an indication of approval by the Examiner.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,
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Dated: December 24, 2002

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1/185

SEQ ID NO: 1

1 GGATCCCAGGGAACGTGACC ATG GTC GTA GGG ATG ACT TGA CAGTTTCAACGGGGTGC GACCACCGTTGCGC 72
1 M V V G M T) * 7

SEQ ID NO: 2
73 TCAGAAGGCATACGTTGGTGAACACGTCGGAAGCTGGGAGGTGAATCTG ATG GCT GGC GAC CAA GAG CTG 144
1 A G D Q E L 7

SEQ ID NO: 3
145 GAA CTG CGG TTC GAC GTT CCT CTT TAC ACG CTT GCC GAG GCA TCG CGG TAC CTG GTG GTT 204
8 E L R F D V P L Y T L A E A S R Y L V V 27

205 CCC CGC GCC ACC CTG GCT ACG TGG GCT GAC GGC TAC GAG CGT CGG CCG GCC AAC GCA CCG 264
28 P R A T L A T W A D G Y E R R P A N A P 47

265 GCG GTC CAG GGG CAA CCG ATC GCC TTT GAC GCC TAT TCG GTC GCG CAG CTT TTT GGC GAC 324
48 A V Q G Q P I A F D A Y S V A Q L F G D 67

325 GTC ACT GGT GCC CGC GTT GCG GGC GTC CAG CCG CAG CGA CAC CAC ATA CCG CCG GTC CCG 384
68 V T G A R V A G V Q P Q R H H I R P V R 87

385 TTG CGG GGG CCG TTG GGT GGG GTT GGG TGC CTC CGT CAC CCC AGG CAG TTC GCT GGC TAT 444
88 L R G P L G G V G C L R H P R Q F A G Y 107

445 TTG TCG CAG TAG CGCGACGGCATTGTCG ATG TCT TGG TAG CTAGCATCCGGTCGGGGGGCCGCTACCAGCG 515
108 L S Q) * M S W * 4

516 CCAGCGCCGGGGCTCCCCGGTCCGGGTAGTGC GCGCTCGAGTTGGTCGTGGACCAGCA ATG ACT GCG ACC CCG 587
1 SEQ ID NO: 5 (M T A T R 5

588 CGA CTT CGA AAC CGC CAC CGG TTA GAT TCC CCG ACT GCG TCA TCG CCA GGT AAA CCG CCG 647
6 R L R N R H R L D S P T A S S P G K P P 25

648 GCA CTA ACG CCA GCA ACC AAC CCG TGA AGACCAACCAACGGGCACCTGCGCAGGTTGCGGCTCAACCGCATC 718
26 A L T P A T N P) * 34

719 ATG AAC TGC TGG ATT TCG GAC TCC CCG TAC TCT CGC GCA GTG CGT GCC CGC GAG CCT ACC 778
1 M N C W I S D S P Y S R A V R A R E P T 20

SEQ ID NO: 6
779 GAA GAT CGC GTG CAT GCG TTC GGC GTG GAC CGC ACA GCA CCT GGA GTT GGC GGC GCC GAG 838
21 E D R V H A F G V D R T A P G V G G A E 40

839 GGC CGA GAT GGC AGG ATG ACG GAT CGT CGG GGG CGG GAA CTC CCA GGC CGC CGG ACC GTC 898
41 G R D G R M T D R R G R E L P G R R T V 60

899 GCA AAC CCG TCG CAA ACC CGT CGC AAA CCG TAA GGAGTCATCC ATG AAG ACA GGC ACC GCG 959
61 A N P S Q T R R K P) * SEQ ID NO: 7 (M K T G T A 6

960 ACG ACG CGG CGC AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG TTG CCG GGG GCC GCC GTT 1019
7 T T R R R L L A V L I A L A L P G A A V 26

1020 GCG CTG CTG GCC GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG TGC GCG GCC AGC GAA GTG 1079
27 A L L A E P S A T G A S D P C A A S E V 46

1080 GCG AGG ACG GTC GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC CTG GAT TCA CAC CCA GAG 1139
47 A R T V G S V A K S M G D Y L D S H P E 66

1140 ACC AAC CAG GTG ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG CCG GGG TCG GTC GCA TCG 1199
67 T N Q V M T A V L Q Q Q V G P G S V A S 86

1200 CTG AAG GCC CAT TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT CC 1243
87 L K A H F E A N P K V A S D) 100

SEQ ID NOS: 1-7

FIGURE 1

2/185

SEQ ID NO:8

Insert of the clone containing DP428 and contained in seq1

1/1 31/11
 → GAT CGC CTT TGA CGC CTA TTC GGT CGC GCA GCT TTT TGG CGA CGT CAC TGG TGC CCG CGT
 asp arg leu OPA (arg leu phe gly arg ala ala phe trp arg arg his trp cys pro arg
 61/21 SEQ ID NO:9 91/31
 TGC GGG CGT CCA GCC GCA GCG ACA CCA CAT ACG GCC GGT CCG GTT GCG GGG GCC GTT GGG
 cys gly arg pro ala ala ala thr pro his thr ala gly pro val ala gly ala val gly
 121/41 151/51
 TGG GGT TGG GTG CCT CCG TCA CCC CAG GCA GTT CGC TGG CTA TTT GTC GCA GTA GCG CGA
 trp gly trp val pro pro ser pro gln ala val arg trp leu phe val ala val ala arg
 181/61 211/71
 CGG CAT TGT CGA TGT CTT GGT AGC TAG CAT CCG GTC GGG GGG CCG CTA CCA GCG CCA GCG
 arg his cys arg cys leu gly ser) AMB (his pro val gly gly pro leu pro ala pro ala
 241/81 SEQ ID NO:10 271/91
 CCG GGG CTC CCC GGT CCG GGT AGT GCG CGT CGA GTT GGT CGT GGA CCA GCA ATG ACT GCG
 pro gly leu pro gly pro gly ser ala arg arg val gly arg gly pro ala met thr ala
 301/101 331/111
 ACC CGG CGA CTT CGA AAC CGC CAC CGG TTA GAT TCC CCG ACT GCG TCA TCG CCA GGT AAA
 thr arg arg leu arg asn arg his arg leu asp ser pro thr ala ser ser pro gly lys
 361/121 391/131
 CCG CCG GCA CTA ACG CCA GCA ACC AAC CCG TGA AGA CCA ACC AAC GGC ACC TGC GCA GGT
 pro pro ala leu thr pro ala thr asn pro) OPA (arg pro thr asn gly thr cys ala gly
 421/141 451/151 SEQ ID NO:11
 TGC GGC TCA ACC GCA TCA TGA ACT GCT GGA TTT CGG ACT CCC CGT ACT CTC GCG CAG TGC
 cys gly ser thr ala ser) OPA (thr ala gly phe arg thr pro arg thr leu ala gln cys
 481/161 SEQ ID NO:12 511/171
 GTG CCC GCG AGC CTA CCG AAG ATC GCG TGC ATG CGT TCG GCG TGG ACC GCA CAG CAC CTG
 val pro ala ser leu pro lys ile ala cys met arg ser ala trp thr ala gln his leu
 541/181 571/191
 GAG TTG GCG GCG CCG AGG GCC GAG ATG GCA GGA TGA CCG ATC GTC GGG GGC GGG AAC TCC
 glu leu ala ala pro arg ala glu met ala gly) OPA (arg ile val gly gly gly asn ser
 601/201 631/211 SEQ ID NO:13
 CAG GCC GCC GGA CCG TCG CAA ACC CGT CGC AAA CCC GTC GCA AAC CGT AAG GAG TCA TCC
 gln ala ala gly pro ser gln thr arg arg lys pro val ala asn arg lys glu ser ser
 661/221 691/231
 ATG AAG ACA GGC ACC GCG ACG ACG CGG CGC AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG
 met lys thr gly thr ala thr thr arg arg arg leu leu ala val leu ile ala leu ala
 721/241 751/251
 TTG CCG GGG GCC GCC GTT GCG CTG CTG GCC GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG
 leu pro gly ala ala val ala leu leu ala glu pro ser ala thr gly ala ser asp pro
 781/261 811/271
 TGC GCG GCC AGC GAA GTG GCG AGG ACG GTC GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC
 cys ala ala ser glu val ala arg thr val gly ser val ala lys ser met gly asp tyr
 841/281 871/291
 CTG GAT TCA CAC CCA GAG ACC AAC CAG GTG ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG
 leu asp ser his pro glu thr asn gln val met thr ala val leu gln gln gln val gly
 901/301 931/311
 CCG GGG TCG GTC GCA TCG CTG AAG GCC CAT TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT C
 pro gly ser val ala ser leu lys ala his phe glu ala asn pro lys val ala ser asp)

SEQ ID: NOS: 8-13

FIGURE 1A'

Insert of the clone containing DP428, other reading frame

2/1

32/11

ATC GCC TTT GAC GCC TAT TCG GTC GCG CAG CTT TTT GGC GAC GTC ACT GGT GCC CGC GTT
ile ala phe asp ala tyr ser val ala gln leu phe gly asp val thr gly ala arg val

62/21

92/31

GCG GGC GTC CAG CCG CAG CGA CAC CAC ATA CGG CCG GTC CGG TTG CGG GGG CCG TTG GGT
ala gly val gln pro gln arg his his ile arg pro val arg leu arg gly pro leu gly

122/41

152/51

GGG GTT GGG TGC CTC CGT CAC CCC AGG CAG TTC GCT GGC TAT TTG TCG CAG TAG CGC GAC
gly val gly cys leu arg his pro arg gln phe ala gly tyr leu ser gln) AMB arg asp

182/61

212/71

GGC ATT GTC GAT GTC TTG GTA GCT AGC ATC CGG TCG GGG GGC CGC TAC CAG CGC CAG CGC
gly ile val asp val leu val ala ser ile arg ser gly gly arg tyr gln arg gln arg

242/81

272/91

CGG GGC TCC CCG GTC CGG GTA GTG CGC GTC GAG TTG GTC GTG GAC CAG CAA TGA CTG CGA
arg gly ser pro val arg val val arg val glu leu val val asp gln gln) OPA leu arg

302/101

332/111

CCC GGC GAC TTC GAA ACC GCC ACC GGT TAG ATT CCC CGA CTG CGT CAT CGC CAG GTA AAC
pro gly asp phe glu thr ala thr gly) AMB (ile pro arg leu arg his arg gln val asn

362/121

392/131

CGC CGG CAC TAA CGC CAG CAA CCA ACC CGT GAA GAC CAA CCA ACG GCA CCT GCG CAG GTT
arg arg his) OCH (arg gln gln pro thr arg glu asp gln pro thr ala pro ala gln val

422/141

452/151

GCG GCT CAA CCG CAT CAT GAA CTG CTG GAT TTC GGA CTC CCC GTA CTC TCG CGC AGT GCG
ala ala gln pro his his glu leu leu asp phe gly leu pro val leu ser arg ser ala

482/161

512/171

TGC CCG CGA GCC TAC CGA AGA TCG CGT GCA TGC GTT CCG CGT GGA CCG CAC AGC ACC TGG
cys pro arg ala tyr arg arg ser arg ala cys val arg arg gly pro his ser thr trp

542/181

572/191

AGT TGG CGG CGC CGA GGG CCG AGA TGG CAG GAT GAC GGA TCG TCG GGG GCG GGA ACT CCC
ser trp arg arg arg gly pro arg trp gln asp asp gly ser ser gly ala gly thr pro)

602/201

632/211

AGG CCG CCG GAC CGT CGC AAA CCC GTC GCA AAC CCG TCG CAA ACC GTA AGG AGT CAT CCA
arg pro pro asp arg arg lys pro val ala asn pro ser gln thr val arg ser his pro

662/221

692/231

TGA AGA CAG GCA CCG CGA CGA CGC GGC GCA GGC TGT TGG CAG TAC TGA TCG CCC TCG CGT
OPA (arg gln ala pro arg arg arg gly ala gly cys trp gln tyr) OPA (ser pro ser arg

722/241

752/251

TGC CGG GGG CCG CCG TTG CGC TGC TGG CCG AAC CAT CAG CGA CCG GCG CGT CGG ACC CGT
cys arg gly pro pro leu arg cys trp pro asn his gln arg pro ala arg arg thr arg

782/261

812/271

GCG CGG CCA GCG AAG TGG CGA GGA CCG TCG GTT CGG TCG CCA AGT CGA TGG GCG ACT ACC
ala arg pro ala lys trp arg gly arg ser val arg ser pro ser arg trp ala thr thr

842/281

872/291

TGG ATT CAC ACC CAG AGA CCA ACC AGG TGA TGA CCG CGG TCT TGC AGC AGC AGG TAG GGC
trp ile his thr gln arg pro thr arg) OPA OPA (pro arg ser cys ser ser arg) AMB (gly

902/301

932/311

CGG GGT CGG TCG CAT CGC TGA AGG CCC ATT TCG AGG CGA ATC CCA AGG TCG CAT CGG ATC
arg gly arg ser his arg) OPA (arg pro ile ser arg arg ile pro arg ser his arg ile)

SEQ ID NO: 24

SEQ ID NOS: 14-24

FIGURE 1B'

SEQ ID NO: 23

SEQ ID NO: 25

Seq1C: Insert of the DP428 clone, other reading frame

3/1

33/11

TCG CCT TTG ACG CCT ATT CGG TCG CGC AGC TTT TTG GCG ACG TCA CTG GTG CCC GCG TTG
 (ser pro leu thr pro ile arg ser arg ser phe leu ala thr ser leu val pro ala leu

63/21

93/31

CGG GCG TCC AGC CGC AGC GAC ACC ACA TAC GGC CGG TCC GGT TGC GGG GGC CGT TGG GTG
 arg ala ser ser arg ser asp thr thr tyr gly arg ser gly cys gly gly arg trp val

123/41

153/51

GGG TTG GGT GCC TCC GTC ACC CCA GGC AGT TCG CTG GCT ATT TGT CGC AGT AGC GCG ACG
 gly leu gly ala ser val thr pro gly ser ser leu ala ile cys arg ser ser ala thr

183/61

213/71

GCA TTG TCG ATG TCT TGG TAG CTA GCA TCC GGT CGG GGG GCC GCT ACC AGC GCC AGC GCC
 ala leu ser met ser trp) AMB (leu ala ser gly arg gly ala ala thr ser ala ser ala

243/81

SEQ ID NO: 27 273/91

GGG GCT CCC CGG TCC GGG TAG TGC GCG TCG AGT TGG TCG TGG ACC AGC AAT GAC TGC GAC
 gly ala pro arg ser gly) AMB (cys ala ser ser trp thr ser asn asp cys asp

303/101

333/111

CCG GCG ACT TCG AAA CCG CCA CCG GTT AGA TTC CCC GAC TGC GTC ATC GCC AGG TAA ACC
 pro ala thr ser lys pro pro pro val arg phe pro asp cys val ile ala arg) OCH (thr

363/121

393/131

SEQ ID NO: 29

GCC GGC ACT AAC GCC AGC AAC CAA CCC GTG AAG ACC AAC CAA CGG CAC CTG CGC AGG TTG
 ala gly thr asn ala ser asn gln pro val lys thr asn gln arg his leu arg arg leu

423/141

453/151

CGG CTC AAC CGC ATC ATG AAC TGC TGG ATT TCG GAC TCC CCG TAC TCT CGC GCA GTG CGT
 arg leu asn arg ile met asn cys trp ile ser asp ser pro tyr ser arg ala val arg

483/161

513/171

GCC CGC GAG CCT ACC GAA GAT CGC GTG CAT GCG TTC GGC GTG GAC CGC ACA GCA CCT GGA
 ala arg glu pro thr glu asp arg val his ala phe gly val asp arg thr ala pro gly

543/181

573/191

GTT GGC GGC GCC GAG GGC CGA GAT GGC AGG ATG ACG GAT CGT CGG GGG CGG GAA CTC CCA
 val gly gly ala glu gly arg asp gly arg met thr asp arg arg gly arg glu leu pro

603/201

633/211

GGC CGC CGG ACC GTC GCA AAC CCG TCG CAA ACC CGT CGC AAA CCG TAA GGA GTC ATC CAT
 gly arg arg thr val ala asn pro ser gln thr arg arg lys pro) OCH (gly val ile his

663/221

693/231

SEQ ID NO: 30

GAA GAC AGG CAC CGC GAC GAC GCG GCG CAG GCT GTT GGC AGT ACT GAT CGC CCT CGC GTT
 glu asp arg his arg asp asp ala ala gln ala val gly ser thr asp arg pro arg val

723/241

753/251

GCC GGG GGC CGC CGT TGC GCT GCT GGC CGA ACC ATC AGC GAC CGG CGC GTC GGA CCC GTG
 ala gly gly arg arg cys ala ala gly arg thr ile ser asp arg arg val gly pro val

783/261

813/271

CGC GGC CAG CGA AGT GGC GAG GAC GGT CGG TTC GGT CGC CAA GTC GAT GGG CGA CTA CCT
 arg gly gln arg ser gly glu asp gly arg phe gly arg gln val asp gly arg leu pro

843/281

873/291

GGA TTC ACA CCC AGA GAC CAA CCA GGT GAT GAC CGC GGT CTT GCA GCA GCA GGT AGG GCC
 gly phe thr pro arg asp gln pro gly asp asp arg gly leu ala ala ala gly arg ala

903/301

933/311

GGG GTC GGT CGC ATC GCT GAA GGC CCA TTT CGA GGC GAA TCC CAA GGT CGC ATC GGA TC
 gly val gly arg ile ala glu gly pro phe arg gly glu ser gln gly arg ile gly)

SEQ ID NOS: 25-30

FIGURE 1C'

Coding sequence DP428 identical to the Rv0203 predicted by Cole et al.
(Nature 393:537-544)

1/1 31/11
 ATG AAG ACA GGC ACC GCG ACG ACG CGG CGC AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG
 Met lys thr gly thr ala thr thr arg arg arg leu leu ala val leu ile ala leu ala
 61/21 91/31
 TTG CCG GGG GCC GCC GTT GCG CTG CTG GCC GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG
 leu pro gly ala ala val ala leu leu ala glu pro ser ala thr gly ala ser asp pro
 121/41 151/51
 TGC GCG GCC AGC GAA GTG GCG AGG ACG GTC GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC
 cys ala ala ser glu val ala arg thr val gly ser val ala lys ser met gly asp tyr
 181/61 211/71
 CTG GAT TCA CAC CCA GAG ACC AAC CAG GTG ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG
 leu asp ser his pro glu thr asn gln val met thr ala val leu gln gln gln val gly
 241/81 271/91
 CCG GGG TCG GTC GCA TCG CTG AAG GCC CAT TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT
 pro gly ser val ala ser leu lys ala his phe glu ala asn pro lys val ala ser asp
 301/101 331/111
 CTG CAC GCG CTT TCG CAA CCG CTG ACC GAT CTT TCG ACT CGG TGC TCG CTG CCG ATC AGC
 leu his ala leu ser gln pro leu thr asp leu ser thr arg cys ser leu pro ile ser
 361/121 391/131
 GGC CTG CAG GCG ATC GGT TTG ATG CAG GCG GTG CAG GGC GCC CGC CGG TAG
 gly leu gln ala ile gly leu met gln ala val gln gly ala arg arg)AMB

SEQ ID NOS: 31-32

FIGURE 1D

ORF containing the DP428 sequence and forming part of seq1A'

1/1 31/11
 TGA CGG ATC GTC GGG GGC GGG AAC TCC CAG GCC GCC GGA CCG TCG CAA ACC CGT CGC AAA
 OPA(arg ile val gly gly gly asn ser gln ala ala gly pro ser gln thr arg arg lys
 61/21 91/31
 CCC GTC GCA AAC CGT AAG GAG TCA TCC ATG AAG ACA GGC ACC GCG ACG ACG CGG CGC AGG
 pro val ala asn arg lys glu ser ser met lys thr gly thr ala thr thr arg arg arg
 121/41 151/51
 CTG TTG GCA GTA CTG ATC GCC CTC GCG TTG CCG GGG GCC GCC GTT GCG CTG CTG GCC GAA
 leu leu ala val leu ile ala leu ala leu pro gly ala ala val ala leu leu ala glu
 181/61 211/71
 CCA TCA GCG ACC GGC GCG TCG GAC CCG TGC GCG GCC AGC GAA GTG GCG AGG ACG GTC GGT
 pro ser ala thr gly ala ser asp pro cys ala ala ser glu val ala arg thr val gly
 241/81 271/91
 TCG GTC GCC AAG TCG ATG GGC GAC TAC CTG GAT TCA CAC CCA GAG ACC AAC CAG GTG ATG
 ser val ala lys ser met gly asp tyr leu asp ser his pro glu thr asn gln val met
 301/101 331/111
 ACC GCG GTC TTG CAG CAG CAG GTA GGG CCG GGG TCG GTC GCA TCG CTG AAG GCC CAT TTC
 thr ala val leu gln gln gln val gly pro gly ser val ala ser leu lys ala his phe
 361/121 391/131
 GAG GCG AAT CCC AAG GTC GCA TCG GAT CTG CAC GCG CTT TCG CAA CCG CTG ACC GAT CTT
 glu ala asn pro lys val ala ser asp leu his ala leu ser gln pro leu thr asp leu
 421/141 451/151
 TCG ACT CGG TGC TCG CTG CCG ATC AGC GGC CTG CAG GCG ATC GGT TTG ATG CAG GCG GTG
 ser thr arg cys ser leu pro ile ser gly leu gln ala ile gly leu met gln ala val
 481/161
 CAG GGC GCC CGC CGG TAG
 gln gly ala arg arg)AMB

SEQ ID NOS: 33-34

FIGURE 1E

SEQ ID NO: 35

191 CCGGTCGGGGGGCCGCTACCAGCGCCAGCGCCGGGGCTCCCCGGTCCGGGTA GTG CGC GTC GAG TTG GTC GTG 563
 1
 564 GAC CAG CAA TGA CTGCGACCCGGCGACTTCGAAACCGCCACCGGTTAGATTCCCCGACTGCGTCATCGCCAGGTAA 639
 8 D Q Q) *
 640 ACCGCGGGCACTAACGCCAGCAACCAACCC GTG AAG ACC AAC CAA CGG CAC CTG CGC AGG TTG CGG 705
 1
 706 CTC AAC CGC ATC ATG AAC TGC TGG ATT TCG GAC TCC CCG TAC TCT CGC GCA GTG CGT GCC 765
 13 L N R I M N C W I S D S P Y S R A V R A 32
 766 CGC GAG CCT ACC GAA GAT CGC GTG CAT GCG TTC GGC GTG GAC CGC ACA GCA CCT GGA GTT 825
 33 R E P T E D R V H A F G V D R T A P G V 52
 826 GGC GGC GCC GAG GGC CGA GAT GGC AGG ATG ACG GAT CGT CGG GGG CGG GAA CTC CCA GGC 885
 53 G G A E G R D G R M T D R R G R E L P G 72
 886 CGC CGG ACC GTC GCA AAC CCG TCG CAA ACC CGT CGC AAA CCG TAA GGAGTCATCC ATG AAG 946
 73 R R T V A N P S Q T R R K P) * xxxxxx (M K 2
 947 ACA GGC ACC GCG ACG ACG CGG CGC AGG CTG TTG GCA GTA CTG ATC GCC CTC GCG TTG CCG 1006
 3 T G T A T T R R R L L A V L I A L A L P 22
 1007 GGG GCC GCC GTT GCG CTG CTG GCC GAA CCA TCA GCG ACC GGC GCG TCG GAC CCG TGC GCG 1066
 23 G A A V A L L A E P S A T G A S D P C A 42
 1067 GCC AGC GAA GTG GCG AGG ACG GTC GGT TCG GTC GCC AAG TCG ATG GGC GAC TAC CTG GAT 1126
 43 A S E V A R T V G S V A K S M G D Y L D 62
 1127 TCA CAC CCA GAG ACC AAC CAG GTG ATG ACC GCG GTC TTG CAG CAG CAG GTA GGG CCG GGG 1186
 63 S H P E T N Q V M T A V L Q Q Q V G P G 82
 1187 TCG GTC GCA TCG CTG AAG GCC CAT TTC GAG GCG AAT CCC AAG GTC GCA TCG GAT CTG CAC 1246
 83 S V A S L K A H F E A N P K V A S D L H 102
 1247 GCG CTT TCG CAA CCG CTG ACC GAT CTT TCG ACT CGG TGC TCG CTG CCG ATC AGC GGC CTG 1306
 103 A L S Q P L T D L S T R C S L P I S G L 122
 1307 CAG GCG ATC GGT TTG ATG CAG GCG GTG CAG GGC GCC CGC CGG TAG ATG CCG GAC CGC CGC 1366
 123 Q A I G L M Q A V Q G A R R) * (M P D R R 5
 1367 CGG GTC CGG CGC AGT CGA CGT GAG GCA GCG GTC GCC TAC CGG GGC GGT GTC TCG CCG CCT 1426
 6 R V R R S R R E A A V A Y R G G V S P P 25
 1427 TCT GGT CGC AGG TCA GGG GTC GGC GCT GGA CCT TGC GGT GTG GTT TCG ACC GGG TCG TCG 1486
 26 S G R R S G V G A G P C G V V S T G S S 45
 1487 CAG GGT GTG CCC TGC GGT TGG ATG ACA AGT CGC AGG TTT GGA TCG GTT GGC GGG TCG CGA 1546
 46 Q G V P C G W M T S R R F G S V G G S R 65
 1547 TCG TTG T 1553
 66 S L) 67

SEQ ID NOS: 35-40

FIGURE 2

SEQ ID NO: 41

SEQ ID NO: 42

31/11
 TCG CCG GCT CGC GGA CGT AGA TAA TAG CTC ACC GTT GGA CGA CCT CGA CAG GGT CCT TTG
 (ser pro ala arg gly arg arg) OCH AMB (leu thr val gly arg pro arg gln gly pro leu)
 61/21
 TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG TCG GGT CAT CGC CTA AGG CTA CCG TTC
 OPA (leu pro gly leu thr arg thr thr thr glu ser gly his arg leu arg leu pro phe)
 121/41
 TGA CCT GGG GTG CGT GGG CGC CGA CGA GTG AGG CAG TCA TGT CTC AGG GCC CAC CGC CAC
 OPA (pro gly val arg gly arg arg arg val arg gln ser cys leu arg ala his arg his
 181/61
 CTC GGT CGC CGG CAG TGT CAG CAT GTG CAG ATG ACT CCA CGC AGC TTG TTC GTG TTG GTG
 leu gly arg arg gln cys gln his val gln met thr pro arg ser leu phe val leu val
 241/81
 TCG TGG TTG CGA CGA CTT GGC GCT GGT GAG CGC ACC CGC CGG CGT CGT GCC GCG CAT GCG
 ser trp leu arg arg leu gly ala gly glu arg thr arg arg arg ala ala his ala
 301/101
 GAT C
 asp)

SEQ ID NO: 43

SEQ ID NO: 44

SEQ ID NO: 45

SEQ ID NOS: 41-45

FIGURE 3A

SEQ ID NO: 46

SEQ ID NO: 47

32/11
 CGC CGG CTC GCG GAC GTA GAT AAT AGC TCA CCG TTG GAC GAC CTC GAC AGG GTC CTT TGT
 (arg arg leu ala asp val asp asn ser ser pro leu asp asp leu asp arg val leu cys
 62/21
 GAC TGC CCG GCT TGA CGC GGA CGA CCA CAG AGT CGG GTC ATC GCC TAA GGC TAC CGT TCT
 asp cys arg ala) OPA (arg gly arg pro gln ser arg val ile ala) OCH (gly tyr arg ser
 122/41
 GAC CTG GGG TGC GTG GGC GCC GAC GAG TGA GGC AGT CAT GTC TCA GGG CCC ACC GCC ACC
 asp leu gly cys val gly ala asp glu) OPA (gly ser his val ser gly pro thr ala thr
 182/61
 TCG GTC GCC GGC AGT GTC AGC ATG TGC AGA TGA CTC CAC GCA GCT TGT TCG TGT TGG TGT
 ser val ala gly ser val ser met cys arg) OPA (leu his ala ala cys ser cys trp cys
 242/81
 CGT GGT TGC GAC GAC TTG GCG CTG GTG AGC GCA CCC GCC GGC GTC GTG CCG CGC ATG CGG
 arg gly cys asp asp leu ala leu val ser ala pro ala gly val val pro arg met arg
 302/101
 ATC
 ile)

SEQ ID NO: 48

SEQ ID NO: 50

SEQ ID NO: 49

SEQ ID NO: 51

SEQ ID NOS: 46-51

FIGURE 3B

SEQ ID NO: 52
 SEQ ID NO: 53

33/11
 GCC GGC TCG CGG ACG TAG ATA ATA GCT CAC CGT TGG ACG ACC TCG ACA GGG TCC TTT GTG
 (ala gly ser arg thr) AMB (ile ile ala his arg trp thr thr ser thr gly ser phe val
 63/21
 ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA GTC GGG TCA TCG CCT AAG GCT ACC GTT CTG
 thr ala gly leu asp ala asp asp his arg val gly ser ser pro lys ala thr val leu
 123/41
 ACC TGG GGT GCG TGG GCG CCG ACG AGT GAG GCA GTC ATG TCT CAG GGC CCA CCG CCA CCT
 thr trp gly ala trp ala pro thr ser glu ala val met ser gln gly pro pro pro pro
 183/61
 CGG TCG CCG GCA GTG TCA GCA TGT GCA GAT GAC TCC ACG CAG CTT GTT CGT GTT GGT GTC
 arg ser pro ala val ser ala cys ala asp asp ser thr gln leu val arg val gly val
 243/81
 GTG GTT GCG ACG ACT TGG CGC TGG TGA GCG CAC CCG CCG GCG TCG TGC CGC GCA TGC GGA
 val val ala thr thr trp arg trp) OPA (ala his pro pro ala ser cys arg ala cys gly)
 TC

SEQ ID NO: 55

SEQ ID NOS: 52-55

FIGURE 3C

SEQ ID NO: 56

SEQ ID NO: 57

31/11
 CCA ATT TTC CTT CGC GCC GTG CAA TAC CAT CTG CAA GAC CAG CGA CGG CCC GTG GTT GCG
 (pro ile phe leu arg ala val gln tyr his leu gln asp gln arg arg pro val val ala
 61/21
 GTC GCG CAG CTT GCG GAA ACC GGG TAT GGA CCC TGC CGT ACC GTT GTT GCC ACT TGA TGT
 val ala gln leu ala glu thr gly tyr gly pro cys arg thr) val val ala thr OPA (cys
 121/41
 CGT CGC TCT CCA CCC GTC GGG GGG CGA AAG CCA TTC CGA CAC TGG GAT CCT CAA AAC GTC
 arg arg ser pro pro val gly gly arg lys pro phe arg his trp asp pro gln asn val
 181/61
 GGC TGA GTG TCT GCA GGG CTC CGG GGA GCA GCC GAT CAT CAC CAT GTA CGA ACT GAA TAA
 gly) OPA (val ser ala gly leu arg gly ala ala asp his his his val arg thr glu) OCH
 241/81
 GTC CCC CGC GCG CGA CTT CCA GAC ATT TGT TGT GGT TTC GGT TGA GGC CGA GGC GAG GCT
 (val pro arg ala arg leu pro asp ile cys cys gly phe gly) OPA (gly arg gly glu ala
 301/101
 CAT TTC GCA GCA ACC GGT CTC CGG GTC GCA GCA TCG TTG CGG CGA TCG CGG CGC AGT CGT
 his phe ala ala thr gly leu arg val ala ala ser leu arg arg ser arg arg ser arg
 361/121
 CGG ACG AGT CGT CGT CAA CGA CCA CGA TC
 arg thr ser arg arg gln arg pro arg)

SEQ ID NO: 60

SEQ ID NOS: 56-61

FIGURE 4A

SEQ ID NO: 62

CAA TTT TCC TTC GCG CCG TGC AAT ACC ATC TGC AAG ACC AGC GAC GGC CCG TGG TTG CGG
 gln(phe ser phe ala pro cys asn thr ile cys lys thr ser asp gly pro trp leu arg
 62/21) SEQ ID NO: 63
 TCG CGC AGC TTG CGG AAA CCG GGT ATG GAC CCT GCC GTA CCG TTG TTG CCA CTT GAT GTC
 ser arg ser leu arg lys pro gly met asp pro ala val pro leu leu pro leu asp val
 122/41
 GTC GCT CTC CAC CCG TCG GGG GGC GAA AGC CAT TCC GAC ACT GGG ATC CTC AAA ACG TCG
 val ala leu his pro ser gly gly glu ser his ser asp thr gly ile leu lys thr ser
 182/61
 GCT GAG TGT CTG CAG GGC TCC GGG GAG CAG CCG ATC ATC ACC ATG TAC GAA CTG AAT AAG
 ala glu cys leu gln gly ser gly glu gln pro ile ile thr met tyr glu leu asn lys
 242/81
 TCC CCC GCG CGC GAC TTC CAG ACA TTT GTT GTG GTT TCG GTT GAG GCC GAG GCG AGG CTC
 ser pro ala arg asp phe gln thr phe val val val ser val glu ala glu ala arg leu
 302/101
 ATT TCG CAG CAA CCG GTC TCC GGG TCG CAG CAT CGT TGC GGC GAT CGC GGC GCA GTC GTC
 ile ser gln gln pro val ser gly ser gln his arg cys gly asp arg gly ala val val
 362/121
 GGA CGA GTC GTC GTC AAC GAC CAC GAT C
 gly arg val val val asn asp his asp)

SEQ ID NOS: 62-63

FIGURE 4B

SEQ ID NO: 64

AAT TTT CCT TCG CGC CGT GCA ATA CCA TCT GCA AGA CCA GCG ACG GCC CGT GGT TGC GGT
 (asn phe pro ser arg arg ala ile pro ser ala arg pro ala thr ala arg gly cys gly
 63/21)
 CGC GCA GCT TGC GGA AAC CGG GTA TGG ACC CTG CCG TAC CGT TGT TGC CAC TTG ATG TCG
 arg ala ala cys gly asn arg val trp thr leu pro tyr arg cys cys his leu met ser
 123/41
 TCG CTC TCC ACC CGT CGG GGG GCG AAA GCC ATT CCG ACA CTG GGA TCC TCA AAA CGT CGG
 ser leu ser thr arg arg gly ala lys ala ile pro thr leu gly ser ser lys arg arg
 183/61
 CTG AGT GTC TGC AGG GCT CCG GGG AGC AGC CGA TCA TCA CCA TGT ACG AAC TGA ATA AGT
 leu ser val cys arg ala pro gly ser ser arg ser ser pro cys thr asn) OPA(ile ser
 243/81
 CCC CCG CGC GCG ACT TCC AGA CAT TTG TTG TGG TTT CGG TTG AGG CCG AGG CGA GGC TCA
 pro pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg arg gly ser
 303/101
 TTT CGC AGC AAC CGG TCT CCG GGT CGC AGC ATC GTT GCG GCG ATC GCG GCG CAG TCG TCG
 phe arg ser asn arg ser pro gly arg ser ile val ala ala ile ala ala gln ser ser
 363/121
 GAC GAG TCG TCG TCA ACG ACC ACG ATC
 asp glu ser ser ser thr thr thr ile)

SEQ ID NO: 66

SEQ ID NOS: 64-66

FIGURE 4C

10/185

part of the nucleotide sequence of seq4A

SEQ ID NO: 67

1/1 31/11
CCG CGC GCG ACT TCC AGA CAT TTG TTG TGG TTT CGG TTG AGG CCG AGG CGA GGC TCA TTT
(pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg arg gly ser phe
61/21 91/31
CGC AGC AAG CGG TCT CCG GGT CGC AGC ATC GTT GCG GCG ATC GCG GCG CAG TCG TCG GAC
arg ser lys arg ser pro gly arg ser ile val ala ala ile ala ala gln ser ser asp
121/41
GAG TCG TCG TCA ACG ACC ACG ATC
glu ser ser ser thr thr thr ile)

SEQ ID NOS: 67-68

FIGURE 4A'

SEQ ID NO: 69

1/1 31/11
CGC GCG CGA CTT CCA GAC ATT TGT TGT GGT TTC GGT TGA GGC CGA GGC GAG GCT CAT TTC
(arg ala arg leu pro asp ile cys cys gly phe gly) OPA (gly arg gly glu ala his phe
61/21 91/31
GCA GCA AGC GGT CTC CGG GTC GCA GCA TCG TTG CGG CGA TCG CGG CGC AGT CGT CGG ACG
ala ala ser gly leu arg val ala ala ser leu arg arg ser arg arg ser arg arg thr
121/41
AGT CGT CGT CAA CGA CCA CGA TC
ser arg arg gln arg pro arg)

SEQ ID NOS: 69-71

FIGURE 4B'

SEQ ID NO: 72

1/1 31/11
GCC GCG CGC GAC TTC CAG ACA TTT GTT GTG GTT TCG GTT GAG GCC GAG GCG AGG CTC ATT
(ala ala arg asp phe gln thr phe val val val ser val glu ala glu ala arg leu ile
61/21 91/31
TCG CAG CAA GCG GTC TCC GGG TCG CAG CAT CGT TGC GGC GAT CGC GGC GCA GTC GTC GGA
ser gln gln ala val ser gly ser gln his arg cys gly asp arg gly ala val val gly
121/41
CGA GTC GTC GTC AAC GAC CAC GAT C
arg val val val asn asp his asp

SEQ ID NOS: 72-73

FIGURE 4C'

11/185

ORF according to Cole et al. (Nature 393:537-544) and containing the sequence Seq 4A'

1/1

31/11

tga ata agt ccg ccg cgc gcg act tcc aga cat ttg ttg tgg ttt cgg ttg agg ccg agg
OPA(ile ser pro pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg

61/21

91/31

cga ggc tca ttt cgc agc aag cgg tct ccg ggt cgc agc atc gtt gcg gcg atc gcg gcg
arg gly ser phe arg ser lys arg ser pro gly arg ser ile val ala ala ile ala ala

121/41

151/51

cag tcg tcg gac gag tcg tcg tca acg acc acg atc tcg aac tcg acg ccc tcc tgt tcg
gln ser ser asp glu ser ser ser thr thr thr ile ser asn ser thr pro ser cys ser

181/61

211/71

agg atg cta cgc aga cag cgc tcg atg gtg gcg ccg ttg ttg tac atc ggg atg cac acc
arg met leu arg arg gln arg ser met val ala pro leu leu tyr ile gly met his thr

241/81

271/91

gag ata agc ggt ttc gcc ggg ttc acc gat acc acg ctt gat gca tca cca ggc acc aca
glu ile ser gly phe ala gly phe thr asp thr thr leu asp ala ser pro gly thr thr

301/101

tgg cga ctc aga gac tag

trp arg leu arg asp)AMB

SEQ ID NOS: 74-75

FIGURE 4D'

sequence upstream of seq4A' and fused with seq4A'

1/1

31/11

GCA ACC TAC CAG CAG AGC CAG GGG CTC ACA GGA CCT AAA GGA GTA GCG CCC ATG GCT GAT
(ala thr tyr gln gln ser gln gly leu thr gly pro lys gly val ala pro met ala asp

C

SEQ ID NOS: 76-77

FIGURE 4E'

seq4J' in another reading frame

1/1

31/11

ACG CAA CCT ACC AGC AGA GCC AGG GGC TCA CAG GAC CTA AAG GAG TAG CGC CCA TGG CTG
(thr gln pro thr ser arg ala arg gly ser gln) asp (leu lys glu AMB arg pro trp leu

61/21

SEQ ID NO: 80

ATC

ile)

SEQ ID NOS: 78-80

FIGURE 4F'

seq 4J' in the third reading frame

1/1

31/11

CGC AAC CTA CCA GCA GAG CCA GGG GCT CAC AGG ACC TAA AGG AGT AGC GCC CAT GGC TGA
(arg asn leu pro ala glu pro gly ala his arg thr) OCH (arg ser ser ala his gly) OPA

SEQ ID NO: 82

SEQ ID NO: 83

TC

SEQ ID NOS: 81-83

FIGURE 4G'

12/185

sequence Rv2050 predicted by Cole et al. (Nature 393:537-544) and containing seq4J

1/1 31/11
 ATG GCT GAT CGT GTC CTG AGG GGC AGT CGC CTC GGA GCC GTG AGC TAT GAG ACC GAC CGC
 (Met ala asp arg val leu arg gly ser arg leu gly ala val ser tyr glu thr asp arg
 61/21 91/31
 AAC CAC GAC CTG GCG CCG CGC CAG ATC GCG CGG TAC CGC ACC GAC AAC GGC GAG GAG TTC
 asn his asp leu ala pro arg gln ile ala arg tyr arg thr asp asn gly glu glu phe
 121/41 151/51
 GAA GTC CCG TTC GCC GAT GAC GCC GAG ATC CCC GGC ACC TGG TTG TGC CGC AAC GGC ATG
 glu val pro phe ala asp asp ala glu ile pro gly thr trp leu cys arg asn gly met
 181/61 211/71
 GAA GGC ACC CTG ATC GAG GGC GAC CTG CCC GAG CCG AAG AAG GTT AAG CCG CCC CGG ACG
 glu gly thr leu ile glu gly asp leu pro glu pro lys lys val lys pro pro arg thr
 241/81 271/91
 CAC TGG GAC ATG CTG CTG GAG CGC CGT TCC ATC GAA GAA CTC GAA GAG TTA CTT AAG GAG
 his trp asp met leu leu glu arg arg ser ile glu glu leu glu glu leu leu lys glu
 301/101 331/111
 CGC CTC GAG CTC ATT CGG TCA CGT CGG CGC GGC TGA
 arg leu glu leu ile arg ser arg arg arg gly)OPA

SEQ ID NOS: 84-85

FIGURE 4H'

ORF according to Cole et al. (Nature 393:537-544) and containing the sequence Rv2050

1/1 31/11
 TAG TCC GCC CGG GTG TCC GAT CCC GGT ATC ATT GAT GGT CGC GCC GCG CGC GTC GCG TGC
 (ser ala arg val ser asp pro gly ile ile asp gly arg ala ala arg val ala cys
 61/21 91/31
 CGG GAA CTA CGC AGA CGG CCG CAG CGT TTG CCA ACC GGA GCC AGT CGC CAG TAC GCA ACC
 arg glu leu arg arg arg pro gln arg leu pro thr gly ala ser arg gln tyr ala thr
 121/41 151/51
 TAC CAG CAG AGC CCA GGG CTC ACA GGA CCT AAA GGA GTA GCG CCC ATG GCT GAT CGT GTC
 tyr gln gln ser pro gly leu thr gly pro lys gly val ala pro met ala asp arg val
 181/61 211/71
 CTG AGG GGC AGT CGC CTC GGA GCC GTG AGC TAT GAG ACC GAC CGC AAC CAC GAC CTG GCG
 leu arg gly ser arg leu gly ala val ser tyr glu thr asp arg asn his asp leu ala
 241/81 271/91
 CCG CGC CAG ATC GCG CGG TAC CGC ACC GAC AAC GGC GAG GAG TTC GAA GTC CCG TTC GCC
 pro arg gln ile ala arg tyr arg thr asp asn gly glu glu phe glu val pro phe ala
 301/101 331/111
 GAT GAC GCC GAG ATC CCC GGC ACC TGG TTG TGC CGC AAC GGC ATG GAA GGC ACC CTG ATC
 asp asp ala glu ile pro gly thr trp leu cys arg asn gly met glu gly thr leu ile
 361/121 391/131
 GAG GGC GAC CTG CCC GAG CCG AAG AAG GTT AAG CCG CCC CGG ACG CAC TGG GAC ATG CTG
 glu gly asp leu pro glu pro lys lys val lys pro pro arg thr his trp asp met leu
 421/141 451/151
 CTG GAG CGC CGT TCC ATC GAA GAA CTC GAA GAG TTA CTT AAG GAG CGC CTC GAG CTC ATT
 leu glu arg arg ser ile glu glu leu glu glu leu leu lys glu arg leu glu leu ile
 481/161
 CGG TCA CGT CGG CGC GGC TGA
 arg ser arg arg arg gly)OPA

SEQ ID NOS: 86-87

FIGURE 4I'

13/185

SEQ ID NO: 88

31/11
 GAT CGC GGT CAA CGA GGC CGA ATA CGG CGA GAT GTG GGC CCA AGA CGC CGC CGC GAT GTT
 asp arg gly gln arg gly arg ile arg arg asp val gly pro arg arg arg arg asp val
 61/21
 TGG CTA CGC CGC GGC GAC GGC GAC GGC GAC GGC GAC GTT GCT GCC GTT CGA GGA GGC GCC
 trp leu arg arg gly asp gly asp gly asp gly asp val ala ala val arg gly gly ala
 121/41
 GGA GAT GAC CAG CGC GGG TGG GCT CCT CGA GCA GGC CGC CGC GGT CGA GGA GGC CTC CGA
 gly asp asp gln arg gly trp ala pro arg ala gly arg arg gly arg gly gly leu arg
 181/61
 CAC CGC CGC GGC GAA CCA GTT GAT GAA CAA TGT GCC CCA GGC GCT GCA ACA GCT GGC CCA
 his arg arg gly glu pro val asp glu gln cys ala pro gly ala ala thr ala gly pro
 241/81
 GCC CAC GCA GGG CAC CAC GCC TTC TTC CAA GCT GGG TGG CCT GTG GAA GAC GGT CTC GCC
 ala his ala gly his his ala phe phe gln ala gly trp pro val glu asp gly leu ala
 301/101
 GCA TCG GTC GCC GAT C
 ala ser val ala asp)

SEQ ID NOS: 88-89

FIGURE 5A

SEQ ID NO: 90

32/11
 ATC GCG GTC AAC GAG GCC GAA TAC GGC GAG ATG TGG GCC CAA GAC GCC GCC GCG ATG TTT
 ile ala val asn glu ala glu tyr gly glu met trp ala gln asp ala ala ala met phe
 62/21
 GGC TAC GCC GCG GCG ACG GCG ACG GCG ACG GCG ACG TTG CTG CCG TTC GAG GAG GCG CCG
 gly tyr ala ala ala thr ala thr ala thr ala thr leu leu pro phe glu glu ala pro
 122/41
 GAG ATG ACC AGC GCG GGT GGG CTC CTC GAG CAG GCC GCC GCG GTC GAG GAG GCC TCC GAC
 glu met thr ser ala gly gly leu leu glu gln ala ala ala val glu glu ala ser asp
 182/61
 ACC GCC GCG GCG AAC CAG TTG ATG AAC AAT GTG CCC CAG GCG CTG CAA CAG CTG GCC CAG
 thr ala ala ala asn gln leu met asn asn val pro gln ala leu gln gln leu ala gln
 242/81
 CCC ACG CAG GGC ACC ACG CCT TCT TCC AAG CTG GGT GGC CTG TGG AAG ACG GTC TCG CCG
 pro thr gln gly thr thr pro ser ser lys leu gly gly leu trp lys thr val ser pro
 302/101
 CAT CGG TCG CCG ATC
 his arg ser pro ile

SEQ ID NOS: 90-91

FIGURE 5B

SEQ ID NO: 92

TCG CGG TCA ACG AGG CCG AAT ACG GCG AGA TGT GGG CCC AAG ACG CCG CCG CGA TGT TTG
 ser (arg ser thr arg pro asn thr ala arg cys gly pro lys thr pro pro arg cys leu
 63/21) ^{SEQ ID NO: 93}
 GCT ACG CCG CGG CGA CGG CGA CGG CGA CGG CGA CGT TGC TGC CGT TCG AGG AGG CGC CGG
 ala thr pro arg arg arg arg arg arg arg arg arg arg cys cys arg ser arg arg arg arg
 123/41
 AGA TGA CCA GCG CGG GTG GGC TCC TCG AGC AGG CCG CCG CGG TCG AGG AGG CCT CCG ACA
 arg) OPA (pro ala arg val gly ser ser ser arg pro pro arg ser arg arg pro pro thr
 183/61) ^{SEQ ID NO: 94}
 CCG CCG CGG CGA ACC AGT TGA TGA ACA ATG TGC CCC AGG CGC TGC AAC AGC TGG CCC AGC
 pro pro arg arg thr ser) OPA OPA (thr met cys pro arg arg cys asn ser trp pro ser
 243/81) ^{SEQ ID NO: 95}
 CCA CGC AGG GCA CCA CGC CTT CTT CCA AGC TGG GTG GCC TGT GGA AGA CGG TCT CGC CGC
 pro arg arg ala pro arg leu leu pro ser trp val ala cys gly arg arg ser arg arg
 303/101
 ATC GGT CGC CGA TC
 ile gly arg arg)

SEQ ID NOS: 92-95

FIGURE 5C

part of the nucleotide sequence Seq 5A

SEQ ID NO: 96

1/1
 CGC CGC GGC GAC GGC GAC GGC GAC GGC GAC GTT GCT GCC GTT CGA GGA GGC GCC GGA GAT
 arg arg gly asp gly asp gly asp gly asp val ala ala val arg gly gly ala gly asp
 61/21
 GAC CAG CGC GGG TGG GCT CCT CGA GCA GGC CGC CGC GGT CGA GGA GGC CTC CGA CAC CGC
 asp gln arg gly trp ala pro arg ala gly arg arg gly arg gly gly leu arg his arg
 121/41
 CGC GGC GAA CCA GTT GAT GAA CAA TGT GCC CCA GGC GCT GCA ACA GCT GGC CCA GCC CAC
 arg gly glu pro val asp glu gln cys ala pro gly ala ala thr ala gly pro ala his
 181/61
 GCA GGG CAC CAC GCC TTC TTC CAA GCT GGG TGG CCT GTG GAA GAC GGT CTC GCC GCA TCG
 ala gly his his ala phe phe gln ala gly trp pro val glu asp gly leu ala ala ser
 241/81
 GTC GCC GAT C
 val ala asp

SEQ ID NO: 97

SEQ ID NOS: 96-97

FIGURE 5A'

SEQ ID NO: 98

1/1 31/11
 TAC GCC GCG GCG ACG GCG ACG GCG ACG GCG ACG TTG CTG CCG TTC GAG GAG GCG CCG GAG
 tyr ala ala ala thr ala thr ala thr ala thr leu leu pro phe glu glu ala pro glu
 61/21 91/31
 ATG ACC AGC GCG GGT GGG CTC CTC GAG CAG GCC GCC GCG GTC GAG GAG GCC TCC GAC ACC
 met thr ser ala gly gly leu leu glu gln ala ala ala val glu glu ala ser asp thr
 121/41 151/51
 GCC GCG GCG AAC CAG TTG ATG AAC AAT GTG CCC CAG GCG CTG CAA CAG CTG GCC CAG CCC
 ala ala ala asn gln leu met asn asn val pro gln ala leu gln gln leu ala gln pro
 181/61 211/71
 ACG CAG GGC ACC ACG CCT TCT TCC AAG CTG GGT GGC CTG TGG AAG ACG GTC TCG CCG CAT
 thr gln gly thr thr pro ser ser lys leu gly gly leu trp lys thr val ser pro his
 241/81
 CGG TCG CCG ATC
 arg ser pro ile

SEQ ID NOS: 98-99

FIGURE 5B'

SEQ ID NO: 100

1/1 31/11
 ACG CCG CGG CGA CGG CGA CGG CGA CGG CGA CGT TGC TGC CGT TCG AGG AGG CGC CGG AGA
 (thr pro arg arg arg arg arg arg arg arg arg arg arg cys cys arg ser arg arg arg arg)
 61/21 91/31
 TGA CCA GCG CGG GTG GGC TCC TCG AGC AGG CCG CCG CGG TCG AGG AGG CCT CCG ACA CCG
 OPA (pro ala arg val gly ser ser ser arg pro pro arg ser arg arg pro pro thr pro
 121/41 151/51
 CCG CGG CGA ACC AGT TGA TGA ACA ATG TGC CCC AGG CGC TGC AAC AGC TGG CCC AGC CCA
 pro arg arg thr ser OPA OPA (thr met cys pro arg arg cys asn ser trp pro ser pro
 181/61 211/71
 CGC AGG GCA CCA CGC CTT CTT CCA AGC TGG GTG GCC TGT GGA AGA CGG TCT CGC CGC ATC
 arg arg ala pro arg leu leu pro ser trp val ala cys gly arg arg ser arg arg ile
 241/81
 GGT CGC CGA TC
 gly arg arg)

SEQ ID NOS: 100-103

FIGURE 5C'

ORF predicted by Cole et al. (Nature 393:537-544) and containing seq5A'

1/1

31/11

SEQ ID NO: 104

tga act gat gat tct gat agc gac caa cct ctt ggg gca aaa cac ccc ggc gat cgc ggt
OPA (thr asp asp ser asp ser asp gln pro leu gly ala lys his pro gly asp arg gly

61/21

SEQ ID NO: 105

91/31

caa cga ggc cga ata cgg cga gat gtg ggc cca aga cgc cgc cgc gat gtt tgg cta cgc
gln arg gly arg ile arg arg asp val gly pro arg arg arg arg asp val trp leu arg
121/41

cgc ggc gac ggc gac ggc gac ggc gac gtt gct gcc gtt cga gga ggc gcc gga gat gac
arg gly asp gly asp gly asp gly asp val ala ala val arg gly gly ala gly asp asp
181/61

cag cgc ggg tgg gct cct cga gca ggc cgc cgc ggt cga gga ggc ctc cga cac cgc cgc
gln arg gly trp ala pro arg ala gly arg arg gly arg gly leu arg his arg arg
241/81

ggc gaa cca gtt gat gaa caa tgt gcc cca ggc gct gca aca gct ggc cca gcc cac gca
gly glu pro val asp glu gln cys ala pro gly ala ala thr ala gly pro ala his ala
301/101

ggg cac cac gcc ttc ttc caa gct ggg tgg cct gtg gaa gac ggt ctc gcc gca tcg gtc
gly his his ala phe phe gln ala gly trp pro val glu asp gly leu ala ala ser val
361/121

gcc gat cag caa cat ggt gtc gat ggc caa caa cca cat gtc gat gac caa ctc ggg tgt
ala asp gln gln his gly val asp gly gln gln pro his val asp asp gln leu gly cys
421/141

gtc gat gac caa cac ctt gag ctc gat gtt gaa ggg ctt tgc tcc ggc ggc ggc cgc cca
val asp asp gln his leu glu leu asp val glu gly leu cys ser gly gly gly arg pro
481/161

ggc cgt gca aac cgc ggc gca aaa cgg ggt ccg ggc gat gag ctc gct ggg cag ctc gct
gly arg ala asn arg gly ala lys arg gly pro gly asp glu leu ala gly gln leu ala
541/181

ggg ttc ttc ggg tct ggg cgg tgg ggt ggc cgc caa ctt ggg tcg ggc ggc ctc ggt cgg
gly phe phe gly ser gly arg trp gly gly arg gln leu gly ser gly gly leu gly arg
601/201

ttc gtt gtc ggt gcc gca ggc ctg ggc cgc ggc caa cca ggc agt cac ccc ggc ggc gcg
phe val val gly ala ala gly leu gly arg gly gln pro gly ser his pro gly gly ala
661/221

ggc gct gcc gct gac cag cct gac cag cgc cgc gga aag agg gcc cgg gca gat gct ggg
gly ala ala ala asp gln pro asp gln arg arg gly lys arg ala arg ala asp ala gly
721/241

cgg gct gcc ggt ggg gca gat ggg cgc cag ggc cgg tgg tgg gct cag tgg tgt gct gcg
arg ala ala gly gly ala asp gly arg gln gly arg trp trp ala gln trp cys ala ala
781/261

tgt tcc gcc gcg acc cta tgt gat gcc gca ttc tcc ggc ggc cgg cta gga gag ggg gcg
cys ser ala ala thr leu cys asp ala ala phe ser gly gly arg leu gly glu gly ala
841/281

cag act gtc gtt att tga
gln thr val val ile) OPA

SEQ ID NOS: 104, 105

FIGURE 5D'

sequence Rv1196 predicted by Cole et al. (Nature 393:537-544) and capable of encoding an ORF fused with Seq5A'

1/1
 atg gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg
 Met val asp phe gly ala leu pro pro glu ile asn ser ala arg met tyr ala gly pro
 61/21 91/31
 ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt
 gly ser ala ser leu val ala ala ala gln met trp asp ser val ala ser asp leu phe
 121/41 151/51
 tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg tcg tgg ata ggt
 ser ala ala ser ala phe gln ser val val trp gly leu thr val gly ser trp ile gly
 181/61 211/71
 tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg tat gtg gcg tgg atg agc gtc acc
 ser ser ala gly leu met val ala
 ala ala ser pro tyr val ala trp met ser val thr
 241/81 271/91
 gcg ggg cag gcc gag ctg acc gcc gcc cag gtc ccg gtt gct gcg gcg gcc tac gag acg
 ala gly gln ala glu leu thr ala ala gln val arg val ala ala ala tyr glu thr
 301/101 331/111
 gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att
 ala tyr gly leu thr val pro pro pro val ile ala glu asn arg ala glu leu met ile
 361/121 391/131
 ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc aac gag gcc gaa
 leu ile ala thr asn leu leu gly gln asn thr pro ala ile ala val asn glu ala glu
 421/141 451/151
 tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg
 tyr gly glu met trp ala gln asp ala ala ala met phe gly tyr ala ala ala thr ala
 481/161 511/171
 acg gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg
 thr ala thr ala thr leu leu pro phe glu glu ala pro glu met thr ser ala gly gly
 541/181 571/191
 ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg
 leu leu glu gln ala ala ala val glu glu ala ser asp thr ala ala ala asn gln leu
 601/201 631/211
 atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag ggc acc acg cct
 met asn asn val pro gln ala leu gln gln leu ala gln pro thr gln gly thr thr pro
 661/221 691/231
 tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg ccg cat cgg tcg ccg atc agc aac
 ser ser lys leu gly gly leu trp lys thr val ser pro his arg ser pro ile ser asn
 721/241 751/251
 atg gtg tcg atg gcc aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac
 met val ser met ala asn asn his met ser met thr asn ser gly val ser met thr asn
 781/261 811/271
 acc ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc gtg caa acc
 thr leu ser ser met leu lys gly phe ala pro ala ala ala ala gln ala val gln thr
 841/281 871/291
 gcg gcg caa aac ggg gtc ccg gcg atg agc tcg ctg ggc agc tcg ctg ggt tct tcg ggt
 ala ala gln asn gly val arg ala met ser ser leu gly ser ser leu gly ser ser gly
 901/301 931/311
 ctg gcc ggt ggg gtg gcc gcc aac ttg ggt ccg gcg gcc tcg gtc ggt tcg ttg tcg gtg
 leu gly gly gly val ala ala asn leu gly arg ala ala ser val gly ser leu ser val
 961/321 991/331
 ccg cag gcc tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg ccg gcg ctg ccg ctg
 pro gln ala trp ala ala ala asn gln ala val thr pro ala ala arg ala leu pro leu
 1021/341 1051/351
 acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg
 thr ser leu thr ser ala ala glu arg gly pro gly gln met leu gly gly leu pro val
 1081/361 1111/371
 ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt gtt ccg ccg cga
 gly gln met gly ala arg ala gly gly gly leu ser gly val leu arg val pro pro arg
 1141/381 1171/391
 ccc tat gtg atg ccg cat tct ccg gcg gcc ggc tag
 pro tyr val met pro his ser pro ala ala gly)AMB

SEQ ID NDS: 106, 107

FIGURE 5E'

Seq 5P: ORF according to Cole et al. (Nature 393:537-544) and containing the sequence Rv1196

1/1
tag gga cac gta atg gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg
AMB (gly his val met val asp phe gly ala leu pro pro glu ile asn ser ala arg met
61/21
tac gcc ggc ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg
tyr ala gly pro gly ser ala ser leu val ala ala ala gln met trp asp ser val ala
121/41
agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg
ser asp leu phe ser ala ala ser ala phe gln ser val val trp gly leu thr val gly
181/61
tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg tat gtg gcg tgg
ser trp ile gly ser ser ala gly leu met val ala ala ala ser pro tyr val ala trp
241/81
atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc gcc cag gtc ccg gtt gct gcg gcg
met ser val thr ala gly gln ala glu leu thr ala ala gln val arg val ala ala ala
301/101
gcc tac gag acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct
ala tyr glu thr ala tyr gly leu thr val pro pro pro val ile ala glu asn arg ala
361/121
gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc
glu leu met ile leu ile ala thr asn leu leu gly gln asn thr pro ala ile ala val
421/141
aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg ttt ggc tac gcc
asn glu ala glu tyr gly glu met trp ala gln asp ala ala ala met phe gly tyr ala
481/161
gcg gcg acg gcg acg gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc
ala ala thr ala thr ala thr ala thr leu leu pro phe glu glu ala pro glu met thr
541/181
agc gcg ggt ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg
ser ala gly gly leu leu glu gln ala ala ala val glu glu ala ser asp thr ala ala
601/201
gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag
ala asn gln leu met asn asn val pro gln ala leu gln gln leu ala gln pro thr gln
661/221
ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg ccg cat cgg tcg
gly thr thr pro ser ser lys leu gly gly leu trp lys thr val ser pro his arg ser
721/241
ccg atc agc aac atg gtg tcg atg gcc aac aac cac atg tcg atg acc aac tcg ggt gtg
pro ile ser asn met val ser met ala asn asn his met ser met thr asn ser gly val
781/261
tcg atg acc aac acc ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag
ser met thr asn thr leu ser ser met leu lys gly phe ala pro ala ala ala ala gln
841/281
gcc gtg caa acc gcg gcg caa aac ggg gtc ccg gcg atg agc tcg ctg ggc agc tcg ctg
ala val gln thr ala ala gln asn gly val arg ala met ser ser leu gly ser ser leu
901/301
ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg ggt ccg gcg gcc tcg gtc ggt
gly ser ser gly leu gly gly gly val ala ala asn leu gly arg ala ala ser val gly
961/321
tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg ccg
ser leu ser val pro gln ala trp ala ala ala asn gln ala val thr pro ala ala arg
1021/341
gcg ctg ccg ctg acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc
ala leu pro leu thr ser leu thr ser ala ala glu arg gly pro gly gln met leu gly
1081/361 1111/371
ggg ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt
gly leu pro val gly gln met gly ala arg ala gly gly gly leu ser gly val leu arg
1141/381
gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gcg gcc ggc tag
val pro pro arg pro tyr val met pro his ser pro ala ala gly AMB

SEQ ID NOS: 108, 109

FIGURE 5F'

SEQ ID NO: 110

31/11
 GGA TCC TGA TGC AAG TGG TCC GGG ATT TGT CGG CAG CCA CCG CGG TCC CGT CGA CCA ACG
 gly ser OPA (cys lys trp ser gly ile cys arg gln pro arg arg ser arg arg pro thr
 61/21
 TTG GTG CAT CCG GGC TGC GAG CAT GCA CGC ACC GAC CAG CGC GGC GAG CGC GGC TAG CTG
 leu val his pro gly cys glu his ala arg thr asp gln arg gly glu arg gly) AMB (leu
 121/41
 CTT GCC CAC TGT TCC TCC CTG CCG GCA CCA TGT GCG ACA AGC TTA AGC GCA GCA GTA CCG
 leu ala his cys ser ser leu pro ala pro cys ala thr ser leu ser ala ala val pro
 181/61
 GCG GTG CCT GGG CAT CCA GCA AAA CGG GGA GCT CAA GAA CGA TTC ATG AAC GAG GGG TCG
 ala val pro gly his pro ala lys arg gly ala gln glu arg phe met asn glu gly sec
 241/81
 TCA CCA ACG TCG AAA CCG ACG GTT GCC AGC CGG CCC ACG ATA TTG CGT GCT CGA GGG TCC
 ser pro thr ser lys pro thr val ala ser arg pro thr ile leu arg ala arg gly ser
 301/101
 GCT GTA CCC TCA CCG AAC GTG AGT CCC ACA CCG CGG AGG CGG GCG ACT CTG GCG TCG TTA
 ala val pro ser pro asn val ser pro thr pro arg arg arg ala thr leu ala ser leu
 361/121
 GCA GCC GAG CTC AAG GTG TCC CGC ACC ACT GTC TCG AAT GCT TTT AAC CGA CCG GAT CCA
 ala ala glu leu lys val ser arg thr thr val ser asn ala phe asn arg pro asp pro
 421/141
 GAA GGA GAA GAT C
 glu gly glu asp)

SEQ ID NOS: 110-112

FIGURE 6A

SEQ ID NO: 113

32/11
 GAT CCT GAT GCA AGT GGT CCG GGA TTT GTC GGC AGC CAC GGC GGT CCC GTC GAC CAA CGT
 asp pro asp ala ser gly pro gly phe val gly ser his gly gly pro val asp gln arg
 62/21
 TGG TGC ATC CGG GCT GCG AGC ATG CAC GCA CCG ACC AGC GCG GCG AGC GCG GCT AGC TGC
 trp cys ile arg ala ala ser met his ala pro thr ser ala ala ser ala ala ser cys
 122/41
 TTG CCC ACT GTT CCT CCC TGC CGG CAC CAT GTG CGA CAA GCT TAA GCG CAG CAG TAC CGG
 leu pro thr val pro pro cys arg his his val arg gln ala) OCH (ala gln gln tyr arg
 182/61
 CGG TGC CTG GGC ATC CAG CAA AAC GGG GAG CTC AAG AAC GAT TCA TGA ACG AGG GGT CGT
 arg cys leu gly ile gln gln asn gly glu leu lys asn asp ser) OPA (thr arg gly arg
 242/81
 CAC CAA CGT CGA AAC CGA CGG TTG CCA GCC GGC CCA CGA TAT TGC GTG CTC GAG GGT CCG
 his gln arg arg asn arg arg leu pro ala gly pro arg tyr cys val leu glu gly pro
 302/101
 CTG TAC CCT CAC CGA ACG TGA GTC CCA CAC CGC GGA GGC GGG CGA CTC TGG CGT CGT TAG
 leu tyr pro his arg thr) OPA (val pro his arg gly gly gly arg leu trp arg arg) AMB
 362/121
 CAG CCG AGC TCA AGG TGT CCC GCA CCA CTG TCT CGA ATG CTT TTA ACC GAC CGG ATC CAG
 gln pro ser ser arg cys pro ala pro leu ser arg met leu leu thr asp arg ile gln
 422/141
 AAG GAG AAG ATC
 lys glu lys ile)

SEQ ID NOS: 113-118

FIGURE 6B

SEQ ID No. 119 33/11
 ATC CTG ATG CAA GTG GTC CGG GAT TTG TCG GCA GCC ACG GCG GTC CCG TCG ACC AAC GTT
 (ile leu met gln val val arg asp leu ser ala ala thr ala val pro ser thr asn val
 SEQ ID No. 120 93/31
 GGT GCA TCC GGG CTG CGA GCA TGC ACG CAC CGA CCA GCG CGG CGA GCG CGG CTA GCT GCT
 gly ala ser gly leu arg ala cys thr his arg pro ala arg arg ala arg leu ala ala
 123/41 153/51
 TGC CCA CTG TTC CTC CCT GCC GGC ACC ATG TGC GAC AAG CTT AAG CGC AGC AGT ACC GGC
 cys pro leu phe leu pro ala gly thr met cys asp lys leu lys arg scr ser thr gly
 183/61 213/71
 GGT GCC TGG GCA TCC AGC AAA ACG GGG AGC TCA AGA ACG ATT CAT GAA CGA GGG GTC GTC
 gly ala trp ala ser ser lys thr gly ser ser arg thr ile his glu arg gly val val
 243/81 273/91
 ACC AAC GTC GAA ACC GAC GGT TGC CAG CCG GCC CAC GAT ATT GCG TGC TCG AGG GTC CGC
 thr asn val glu thr asp gly cys gln pro ala his asp ile ala cys ser arg val arg
 303/101 333/111
 TGT ACC CTC ACC GAA CGT GAG TCC CAC ACC GCG GAG GCG GGC GAC TCT GGC GTC GTT AGC
 cys thr leu thr glu arg glu ser his thr ala glu ala gly asp ser gly val val ser
 363/121 393/131
 AGC CGA GCT CAA GGT GTC CCG CAC CAC TGT CTC GAA TGC TTT TAA CCG ACC GGA TCC AGA
 ser arg ala gln gly val pro his his cys leu glu cys phe) OCH (pro thr gly ser arg
 423/141
 AGG AGA AGA TC
 arg arg arg)

SEQ ID No. 121

SEQ ID Nos. 119-121

FIGURE 6C

SEQ ID No. 122 31/11
 CCG TCG GCA ACT TGG CCG CTG AGG TCG GCT TGA TCC CTG GGC CGA GGC GGG TCA GCC AAT
 (pro ser ala thr trp pro leu arg ser ala) OPA (ser leu gly arg gly gly ser ala asn
 61/21 91/31
 SEQ ID No. 123
 AGC GGC TCC ATC GGC TTT GCT GGT AGC GGT TCG GCG GGA AGC TAG CGG CGA CGT TGT CGG
 ser gly ser ile gly phe ala gly ser gly ser ala gly ser) AMB (arg arg arg cys arg
 121/41 151/51
 TGG CCG GTG ATA TAT TCG GTC AGA CGG GTA TGG CCG CGG CTG AGG TGA TCT GCG ACA CGC
 trp pro val ile tyr trp val arg arg val trp arg arg leu arg) OPA (ser ala thr arg
 181/61 211/71
 CGC CGC GGT GCT CGA GCC AGG CTT ACG ACC AGG GAA TTT CGA AAA TGT TAT TCA GAA CAT
 arg arg gly ala arg ala arg leu thr thr arg glu phe arg lys cys tyr ser glu his
 241/81 271/91
 CTT GTA TCT CTT CTC CGT GCC ACC CCC TAG GTG TAG TGT TTT CGA GTA CCG GCA GAT CCC
 leu val ser leu leu arg ala thr pro) AMB (cys phe arg val pro ala asp pro
 301/101
 AGG TTC ACC AGG TCT CAC CAG ATC
 arg phe thr arg ser his gln ile)

SEQ ID No. 127

SEQ ID Nos. 122-127

FIGURE 7A

SEQ ID No. 128
 CGT CGG CAA CTT GGC CGC TGA GGT CGG CTT GAT CCC TGG GCC GAG GCG GGT CAG CCA ATA
 (arg arg gln leu gly arg) OPA (gly arg leu asp pro trp ala glu ala gly gln pro ile
 SEQ ID No. 129 62/21
 GCG GCT CCA TCG GCT TTG CTG GTA GCG GTT CGG CGG GAA GCT AGC GGC GAC GTT GTC GGT
 ala ala pro ser ala leu leu val ala val arg arg glu ala ser gly asp val val gly
 122/41
 GGC CGG TGA TAT ATT GGG TCA GAC GGG TAT GGC GGC GGC TGA GGT GAT CTG CGA CAC GCC
 gly arg) OPA (tyr ile gly ser asp gly tyr gly gly gly) OPA (gly asp leu arg his ala
 182/61
 GCC GCG GTG CTC GAG CCA GGC TTA CGA CCA GGG AAT TTC GAA AAT GTT ATT CAG AAC ATC
 ala ala val leu glu pro gly leu arg pro gly asn phe glu asn val ile gln asn ile
 242/81
 TTG TAT CTC TTC TCC GTG CCA CCC CCT AGG TGT AGT GTT TTC GAG TAC CGG CAG ATC CCA
 leu tyr leu phe ser val pro pro pro arg cys ser val phe glu tyr arg gln ile pro
 302/101
 GGT TCA CCA GGT CTC ACC AGA TC
 gly ser pro gly leu thr arg)

SEQ ID Nos. 128-132

FIGURE 7B

SEQ ID No. 133
 GTC GGC AAC TTG GCC GCT GAG GTC GGC TTG ATC CCT GGG CCG AGG CGG GTC AGC CAA TAG
 (val gly asn leu ala ala glu val gly leu ile pro gly pro arg arg val ser gln) AMB
 SEQ ID No. 134 63/21
 CGG CTC CAT CGG CTT TGC TGG TAG CGG TTC GGC GGG AAG CTA GCG GCG ACG TTG TCG GTG
 (arg leu his arg leu cys trp) AMB (arg phe gly gly lys leu ala ala thr leu ser val
 123/41
 GCC GGT GAT ATA TTG GGT CAG ACG GGT ATG GCG GCG GCT GAG GTG ATC TGC GAC ACG CCG
 ala gly asp ile leu gly gln thr gly met ala ala ala glu val ile cys asp thr pro
 183/61
 CCG CGG TGC TCG AGC CAG GCT TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC AGA ACA TCT
 pro arg cys ser ser gln ala tyr asp gln gly ile ser lys met leu phe arg thr ser
 243/81
 TGT ATC TCT TCT CCG TGC CAC CCC CTA GGT GTA GTG TTT TCG AGT ACC GGC AGA TCC CAG
 cys ile ser ser pro cys his pro leu gly val val phe ser ser thr gly arg ser gln
 303/101
 GTT CAC CAG GTC TCA CCA GAT C
 val his gln val ser pro asp)

SEQ ID Nos. 133-136

FIGURE 7C

22/185

SEQ ID No. 137

SEQ ID No. 138

31/11
CTT TGC GTG ATG TCC AAT GGC GAA AAC GAC GCC TTG TCA TCG CAA TCG TCA GCA CCG GCC
(leu cys val met ser asn gly glu asn asp ala leu ser ser gln ser ser ala pro ala)
61/21
TAG TTT TCG CGA TGA CGC TCG TTC TGA CCG GAC TTG TGA ACG GGT TTC GGG TCG AGG CCG
AMB phe ser arg OPA arg ser phe OPA pro asp leu OPA (thr gly phe gly ser arg pro
121/41
AGC GAA CCG TCG ATT CCA TGG GTG TCG ACG CAT TCG TGG TCA AGG CCG GCG CCG CAG GAC
ser glu pro ser ile pro trp val ser thr his ser trp ser arg pro ala arg gln asp
181/61
CGT TCC TGG GTT CGA CAC CAT TCG CCC AAA TCG ACC TGC CCC AGG TTG CTC GTG CGC CTG
arg ser trp val arg his his ser pro lys ser thr cys pro arg leu leu val arg leu
241/81
GCG TCT TGG CTG CCG CCC CAC TAG CGA CTG CGC CGT CGA CGA TCC GGC AGG GCA CGT CAG
ala ser trp leu pro pro his) AMB (arg leu arg arg arg arg ser gly arg ala arg gln
301/101
CGC GAA ACG TCA CCG CGT TCG GGG CAC CAG AGC ACG GAC CCG GCA TGC CGC GGG TCT CGG
arg glu thr ser pro arg ser gly his gln ser thr asp pro ala cys arg gly ser arg
361/121
ACG GTC GGG CGC CAT CGA CGC CGG ACG AGG TCG CGG TGT CGA GCA CGC TGG GCC GAA ACC
thr val gly arg his arg arg arg thr arg ser arg cys arg ala arg trp ala glu thr
421/141
TCG GCG ACG ATC
ser ala thr ile)

SEQ ID No. 272

SEQ ID No. 273

SEQ ID Nos. 137-138, 272-273

FIGURE 8A

SEQ ID No. 139

32/11
TTT GCG TGA TGT CCA ATG GCG AAA ACG ACG CCT TGT CAT CGC AAT CGT CAG CAC CGG CCT
phe ala OPA (cys pro met ala lys thr thr pro cys his arg asn arg gln his arg pro
62/21
AGT TTT CCG GAT GAC GCT CGT TCT GAC CGG ACT TGT GAA CGG GTT TCG GGT CGA GGC CGA
ser phe arg asp asp ala arg ser asp arg thr cys glu arg val ser gly arg gly arg
122/41
GCG AAC CGT CGA TTC CAT GGG TGT CGA CGC ATT CGT GGT CAA GGC CGG CGC GGC AGG ACC
ala asn arg arg phe his gly cys arg arg ile arg gly gln gly arg arg gly arg thr
182/61
GTT CCT GGG TTC GAC ACC ATT CGC CCA AAT CGA CCT GCC CCA GGT TGC TCG TGC GCC TGG
val pro gly phe asp thr ile arg pro asn arg pro ala pro gly cys ser cys ala trp
242/81
CGT CTT GGC TGC CGC CCC ACT AGC GAC TGC GCC GTC GAC GAT CCG GCA GGG CAC GTC AGC
arg leu gly cys arg pro thr ser asp cys ala val asp asp pro ala gly his val ser
302/101
GCG AAA CGT CAC CGC GTT CGG GGC ACC AGA GCA CGG ACC CGG CAT GCC GCG GGT CTC GGA
ala lys arg his arg val arg gly thr arg ala arg thr arg his ala ala gly leu gly
362/121
CGG TCG GGC GCC ATC GAC GCC GGA CGA GGT CGC GGT GTC GAG CAC GCT GGG CCG AAA CCT
arg ser gly ala ile asp ala gly arg gly arg gly val glu his ala gly pro lys pro
422/141
CGG CGA CGA TC
arg arg arg)

SEQ ID Nos. 139-140

FIGURE 8B

23/185

ED ID No. 141
 142
 63/21
 123/41
 183/61
 243/81
 303/101
 363/121
 423/141
 GGC GAC GAT C
 gly asp asp)

33/11
 93/31
 153/51
 213/71
 273/91
 333/111
 393/131

TTG CGT GAT GTC CAA TGG CGA AAA CGA CGC CTT GTC ATC GCA ATC GTC AGC ACC GGC CTA
 leu arg asp val gln trp arg lys arg arg leu val ile ala ile val ser thr gly leu
 GTT TTC GCG ATG ACG CTC GTT CTG ACC GGA CTT GTG AAC GGG TTT CGG GTC GAG GCC GAG
 val phe ala met thr leu val leu thr gly leu val asn gly phe arg val glu ala glu
 CGA ACC GTC GAT TCC ATG GGT GTC GAC GCA TTC GTG GTC AAG GCC GGC GCG GCA GGA CCG
 arg thr val asp ser met gly val asp ala phe val val lys ala gly ala ala gly pro
 TTC CTG GGT TCG ACA CCA TTC GCC CAA ATC GAC CTG CCC CAG GTT GCT CGT GCG CCT GGC
 phe leu gly ser thr pro phe ala gln ile asp leu pro gln val ala arg ala pro gly
 GTC TTG GCT GCC GCC CCA CTA GCG ACT GCG CCG TCG ACG ATC CGG CAG GGC ACG TCA GCG
 val leu ala ala ala pro leu ala thr ala pro ser thr ile arg gln gly thr ser ala
 CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC GGA CCC GGC ATG CCG CGG GTC TCG GAC
 arg asn val thr ala phe gly ala pro glu his gly pro gly met pro arg val ser asp
 GGT CGG GCG CCA TCG ACG CCG GAC GAG GTC GCG GTG TCG AGC ACG CTG GGC CGA AAC CTC
 gly arg ala pro ser thr pro asp glu val ala val ser ser thr leu gly arg asn leu
 GGC GAC GAT C
 gly asp asp)

SEQ ID : Nos. 141-142

FIGURE 8C

part of the nucleotide sequence of seq8A

1/1
 61/21
 121/41
 181/61

31/11
 91/31
 151/51

ED ID No. 143
 144
 145

CAG GTT GCT CGT GCG CCT GGC GTC TTG GCT GCC GCC CCA CTA GCG ACT GCG CCG TCG ACG
 (gln val ala arg ala pro gly val leu ala ala ala pro leu ala thr ala pro ser thr
 ATC CGG CAG GGC ACG TCA GCG CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC GGA CCC
 ile arg gln gly thr ser ala arg asn val thr ala phe gly ala pro glu his gly pro
 GGC ATG CCG CGG GTC TCG GAC GGT CGG GCG CCA TCG ACG CCG GAC GAG GTC GCG GTG TCG
 gly met pro arg val ser asp gly arg ala pro ser thr pro asp glu val ala val ser
 AGC ACG CTG GGC CGA AAC CTC GGC GAC GAT C
 ser thr leu gly arg asn leu gly asp asp)

SEQ ID : Nos. 143-144

FIGURE 8A'

SEQ ID No 145 → 1/1
 (arg leu leu val arg leu ala ser trp leu pro pro his) AMB (arg leu arg arg arg arg
 61/21
 TCC GGC AGG GCA CGT CAG CGC GAA ACG TCA CCG CGT TCG GGG CAC CAG AGC ACG GAC CCG
 ser gly arg ala arg gln arg glu thr ser pro arg ser gly his gln ser thr asp pro
 121/41
 GCA TGC CGC GGG TCT CGG ACG GTC GGG CGC CAT CGA CGC CGG ACG AGG TCG CGG TGT CGA
 ala cys arg gly ser arg thr val gly arg his arg arg arg thr arg ser arg cys arg
 181/61
 GCA CGC TGG GCC GAA ACC TCG GCG ACG ATC
 ala arg trp ala glu thr ser ala thr ile)

SEQ ID Nos. 145-147

FIGURE 8B'

Seq8C

SEQ ID No. 148 → 1/1
 (pro gly cys ser cys ala trp arg leu gly cys arg pro thr ser asp cys ala val asp
 61/21
 GAT CCG GCA GGG CAC GTC AGC GCG AAA CGT CAC CGC GTT CGG GGC ACC AGA GCA CGG ACC
 asp pro ala gly his val ser ala lys arg his arg val arg gly thr arg ala arg thr
 121/41
 CGG CAT GCC GCG GGT CTC GGA CGG TCG GGC GCC ATC GAC GCC GGA CGA GGT CGC GGT GTC
 arg his ala ala gly leu gly arg ser gly ala ile asp ala gly arg gly arg gly val
 181/61
 GAG CAC GCT GGG CCG AAA CCT CGG CGA CGA TC
 glu his ala gly pro lys pro arg arg arg)

SEQ ID Nos. 148-149

FIGURE 8C'

sequence Rv2563 predicted by Cole et al. (Nature 393:537-544) and containing seq8A'

atg

met

121/41

151/51

ctt ttt gcg gct ttg cgt gat gtc caa tgg cga aaa cga cgc ctt gtc atc gca atc gtc

(leu phe ala ala leu arg asp val gln trp arg lys arg arg leu val ile ala ile val

181/61

211/71

agc acc ggc cta gtt ttc gcg atg acg ctc gtt ctg acc gga ctt gtg aac ggg ttt cgg

ser thr gly leu val phe ala met thr leu val leu thr gly leu val asn gly phe arg

241/81

271/91

gtc gag gcc gag cga acc gtc gat tcc atg ggt gtc gac gca ttc gtg gtc aag gcc ggc

val glu ala glu arg thr val asp ser met gly val asp ala phe val val lys ala gly

301/101

331/111

gcg gca gga ccg ttc ctg ggt tcg aca cca ttc gcc caa atc gac ctg ccc cag gtt gct

ala ala gly pro phe leu gly ser thr pro phe ala gln ile asp leu pro gln val ala

361/121

391/131

cgt gcg cct ggc gtc ttg gct gcc gcc cca cta gcg act gcg ccg tcg acg atc cgg cag

arg ala pro gly val leu ala ala ala pro leu ala thr ala pro ser thr ile arg gln

421/141

451/151

ggc acg tca gcg cga aac gtc acc gcg ttc ggg gca cca gag cac gga ccc ggc atg ccg

gly thr ser ala arg asn val thr ala phe gly ala pro glu his gly pro gly met pro

481/161

511/171

cgg gtc tcg gac ggt cgg gcg cca tcg acg ccg gac gag gtc gcg gtg tcg agc acg ctg

arg val ser asp gly arg ala pro ser thr pro asp glu val ala val ser ser thr leu

541/181

571/191

ggc cga aac ctc ggc gac gat ctg caa gtg ggt gcg cgc act ttg cgg atc gtc ggc atc

gly arg asn leu gly asp asp leu gln val gly ala arg thr leu arg ile val gly ile

601/201

631/211

gtg ccc gag tca acc gcg ctg gca aag att ccc aac atc ttc ctg acc acc gaa ggc cta

val pro glu ser thr ala leu ala lys ile pro asn ile phe leu thr thr glu gly leu

661/221

691/231

cag cag ttg gca tac aac gga cag ccg aca atc agt tcg atc ggg atc gac ggg atg ccc

gln gln leu ala tyr asn gly gln pro thr ile ser ser ile gly ile asp gly met pro

721/241

751/251

cga cag ctc ccg gac ggc tat cag acc gtc aat cga gcg gat gct gtc agc gat ctg atg

arg gln leu pro asp gly tyr gln thr val asn arg ala asp ala val ser asp leu met

781/261

811/271

cgc ccg ttg aag gtc gcg gtg gat gcg atc acg gtt gtg gcg gtc ttg ctg tgg atc gtt

arg pro leu lys val ala val asp ala ile thr val val ala val leu leu trp ile val

841/281

871/291

gcg gcg ttg atc gtc ggc tcg gtg gtc tac ctc tct gcg ttg gag ccg ctg cgt gac ttt

ala ala leu ile val gly ser val val tyr leu ser ala leu glu arg leu arg asp phe

901/301

931/311

gcg gtg ttc aag gcg atc ggc gtg ccg acg cgc tcg att ctg gcc ggg ctg gcg ctg cag

ala val phe lys ala ile gly val pro thr arg ser ile leu ala gly leu ala leu gln

961/321

991/331

gcg gtc gtc gtc gcg ctg ctc gcg gcg gtg gtt ggc ggc atc ctt tcg ctg ctg ttg gcg

ala val val val ala leu leu ala ala val val gly gly ile leu ser leu leu leu ala

1021/341

1051/351

ccg ttg ttc ccg atg act gtc gtg gta ccc ctg agt gcc ttc gtg gcg cta ccg gcg atc

pro leu phe pro met thr val val val pro leu ser ala phe val ala leu pro ala ile

1081/361

1111/371

gcg act gtg atc ggt ctg ctg gcc agc gtc gca gga ctg ccg cgc gtg gtg gcg atc gat

ala thr val ile gly leu leu ala ser val ala gly leu arg arg val val ala ile asp

1141/381

ccg gca cta gcg ttc gga ggt ccc tag

pro ala leu ala phe gly gly pro AMB)

26/185

ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv2563

1/1

31/11

tag gtt tca aga agg cct gtg cag gtt tcc gca gcc tgg gcc gcg gcg cca ccg aag agc

AMB (val ser arg arg pro val gln val ser ala ala trp ala ala ala pro pro lys ser

61/21 91/31

ccg ccg aaa tgg gct aat ccg gtt cgc ttg gct cga tgc ccg atg atc tgc acc gcc acg

pro pro lys trp ala asn arg val arg leu ala arg ser pro met ile ser thr ala thr

121/41 151/51

acc gac ccc ctc acc tgc gtc gaa cct ccg cga acc aac gcg gca acg cca gcc cat gat

thr asp pro leu thr ser val glu pro arg arg thr asn ala ala thr pro ala his asp

181/61 211/71

cat ttg att ggg tcc acg gaa gca ggt agc ttc cgt cgc atg ctt ttt gcg gct ttg cgt

his leu ile gly ser thr glu ala gly ser phe arg arg met leu phe ala ala leu arg

241/81 271/91

gat gtc caa tgg cga aaa cga cgc ctt gtc atc gca atc gtc agc acc ggc cta gtt ttc

asp val gln trp arg lys arg arg leu val ile ala ile val ser thr gly leu val phe

301/101 331/111

gcg atg acg ctc gtt ctg acc gga ctt gtg aac ggg ttt ccg gtc gag gcc gag cga acc

ala met thr leu val leu thr gly leu val asn gly phe arg val glu ala glu arg thr

361/121 391/131

gtc gat tcc atg ggt gtc gac gca ttc gtg gtc aag gcc ggc gcg gca gga ccg ttc ctg

val asp ser met gly val asp ala phe val val lys ala gly ala ala gly pro phe leu

421/141 451/151

ggt tgc aca cca ttc gcc caa atc gac ctg ccc cag gtt gct cgt gcg cct ggc gtc ttg

gly ser thr pro phe ala gln ile asp leu pro gln val ala arg ala pro gly val leu

481/161 511/171

gct gcc gcc cca cta gcg act gcg ccg tgc acg atc ccg cag ggc acg tca gcg cga aac

ala ala ala pro leu ala thr ala pro ser thr ile arg gln gly thr ser ala arg asn

541/181 571/191

gtc acc gcg ttc ggg gca cca gag cac gga ccc ggc atg ccg ccg gtc tgc gac ggt ccg

val thr ala phe gly ala pro glu his gly pro gly met pro arg val ser asp gly arg

601/201 631/211

gcg cca tgc acg ccg gac gag gtc gcg gtg tgc agc acg ctg ggc cga aac ctc ggc gac

ala pro ser thr pro asp glu val ala val ser ser thr leu gly arg asn leu gly asp

661/221 691/231

gat ctg caa gtg ggt gcg cgc act ttg ccg atc gtc ggc atc gtg ccc gag tca acc gcg

asp leu gln val gly ala arg thr leu arg ile val gly ile val pro glu ser thr ala

721/241 751/251

ctg gca aag att ccc aac atc ttc ctg acc acc gaa ggc cta cag cag ttg gca tac aac

leu ala lys ile pro asn ile phe leu thr thr glu gly leu gln gln leu ala tyr asn

781/261 811/271

gga cag ccg aca atc agt tgc atc ggg atc gac ggg atg ccc cga cag ctc ccg gac ggc

gly gln pro thr ile ser ser ile gly ile asp gly met pro arg gln leu pro asp gly

841/281 871/291

tat cag acc gtc aat cga gcg gat gct gtc agc gat ctg atg cgc ccg ttg aag gtc gcg

tyr gln thr val asn arg ala asp ala val ser asp leu met arg pro leu lys val ala

901/301 931/311

gtg gat gcg atc acg gtt gtg gcg gtc ttg ctg tgg atc gtt gcg gcg ttg atc gtc ggc

val asp ala ile thr val val ala val leu leu trp ile val ala ala leu ile val gly

961/321 991/331

tcg gtg gtc tac ctc tct gcg ttg gag ccg ctg cgt gac ttt gcg gtg ttc aag gcg atc

ser val val tyr leu ser ala leu glu arg leu arg asp phe ala val phe lys ala ile

1021/341 1051/351

ggc gtg ccg acg cgc tgc att ctg gcc ggg ctg gcg ctg cag gcg gtc gtc gtc gcg ctg

gly val pro thr arg ser ile leu ala gly leu ala leu gln ala val val val ala leu

1081/361 1111/371

ctc gcg gcg gtg gtt ggc ggc atc ctt tgc ctg ctg ttg gcg ccg ttg ttc ccg atg act

leu ala ala val val gly gly ile leu ser leu leu leu ala pro leu phe pro met thr

1141/381 1171/391

gtc gtg gta ccc ctg agt gcc ttc gtg gcg cta ccg gcg atc gcg act gtg atc ggt ctg

val val val pro leu ser ala phe val ala leu pro ala ile ala thr val ile gly leu

1201/401 1231/411

ctg gcc agc gtc gca gga ctg ccg cgc gtg gtg gcg atc gat ccg gca cta gcg ttc gga

leu ala ser val ala gly leu arg arg val val ala ile asp pro ala leu ala phe gly

1261/421

ggt ccc tag

gly pro) AMB

SEQ ID: 1005.152-153

FIGURE 8E

sequence of Rv0072 predicted by Cole et al. (Nature 393:537-544) and exhibiting more than 77% similarity with Seq8D'

EO ID No. 154
3EO ID No. 155

1/1	31/11
atg ctc ttc gcg gcc ctg cgt gac atg caa	tgg aga aag cgc cgc ctg gtc atc acg atc
(Met leu phe ala ala leu arg asp met gln	trp arg lys arg arg leu val ile thr ile
61/21	91/31
atc agc acc ggg ctg atc ttc ggg atg acg	ctt gtt ttg acc gga ctc gcg aac ggc ttc
ile ser thr gly leu ile phe gly met thr	leu val leu thr gly leu ala asn gly phe
121/41	151/51
cgg gtg gag gcc cgg cac acc gtc gat tcc	atg ggt gtc gat gta ttc gtc gtc aga tcc
arg val glu ala arg his thr val asp ser	met gly val asp val phe val val arg ser
181/61	211/71
ggc gct gct gga cct ttt ctg ggt tca ata	ccg ttt ccc gat gtt gac ctg gcc cga gtg
gly ala ala gly pro phe leu gly ser ile	pro phe pro asp val asp leu ala arg val
241/81	271/91
gcc gct gaa ccc ggt gtc atg gcc gcg gcc	ccg ttg ggc agc gtg ggg acg atc atg aaa
ala ala glu pro gly val met ala ala ala	pro leu gly ser val gly thr ile met lys
301/101	331/111
gaa ggc acg tcg acg cga aac gtc acg gtc	ttc ggc gcg ccc gag cac gga cct ggc atg
glu gly thr ser thr arg asn val thr val	phe gly ala pro glu his gly pro gly met
361/121	391/131
cca cgg gtc tca gag ggt cgg tca ccg tcg	aaa ccg gac gaa gtc gcg gca tcg agc acg
pro arg val ser glu gly arg ser pro ser	lys pro asp glu val ala ala ser ser thr
421/141	451/151
atg ggc cga cac ctc ggt gac act gtc gag	gtc ggc gcg cgc aga ttg cgg gtc gtt ggc
met gly arg his leu gly asp thr val glu	val gly ala arg arg leu arg val val gly
481/161	511/171
att gtg ccg aat tcc acc gcg ctg gcc aag	atc ccc aat gtc ttc ctc acg acc gag ggc
ile val pro asn ser thr ala leu ala lys	ile pro asn val phe leu thr thr glu gly
541/181	571/191
tta cag aaa ttg gcg tac aac ggg cag ccg	aat atc acg tcc atc ggg atc ata ggt atg
leu gln lys leu ala tyr asn gly gln pro	asn ile thr ser ile gly ile ile gly met
601/201	631/211
ccc cga cag ctg ccg gag ggt tac cag act	ttc gat ccg gtg ggc gct gtc aat gat ttg
pro arg gln leu pro glu gly tyr gln thr	phe asp arg val gly ala val asn asp leu
661/221	691/231
gtg cgc cca ttg aag gtc gca gtg aat tcg	atc tcg atc gtg gct gtt ttg ctg tgg att
val arg pro leu lys val ala val asn ser	ile ser ile val ala val leu leu trp ile
721/241	751/251
gtg gcg gtg ctg atc gtc ggc tcg gtg gtg	tac ctt tcg gct ctt gag cgg cta cgt gac
val ala val leu ile val gly ser val val	tyr leu ser ala leu glu arg leu arg asp
781/261	811/271
ttc gcg gtg ttc aag gcg att ggc acg cca	acg cgc tcg att atg gcc ggg ctc gca tta
phe ala val phe lys ala ile gly thr pro	thr arg ser ile met ala gly leu ala leu
841/281	871/291
cag gcg ctg gtc att gcg ttg ctt gcg gcg	gtg gtg ggc gtc gtc ctg gcg cag gtg ttg
gln ala leu val ile ala leu leu ala ala	val val gly val val leu ala gln val leu
901/301	931/311
gca cca ctg ttt ccg atg att gtc gcg gta	ccc gtc ggt gct tac ctg gcg cta ccg gtg
ala pro leu phe pro met ile val ala val	pro val gly ala tyr leu ala leu pro val
961/321	991/331
gcc gcg atc gtc atc ggt ctg ttc gct agt	gtt gcc gga ttg aag cgc gtg gtg acg gtc
ala ala ile val ile gly leu phe ala ser	val ala gly leu lys arg val val thr val
1021/341	
gat ccc gcg cag gcg ttc gga ggt ccc tag	
asp pro ala gln ala phe gly gly pro) AMB	

SEQ ID Nos 154-155

FIGURE 8F

Seq8H : ORF predicted by Cole et al. (Nature 393:537-544) and containing seq8G
1/1 31/11

tag cct ctg gga atg ctc ttc gcg gcc ctg cgt gac atg caa tgg aga aag cgc cgc ctg
 AMB (pro leu gly met leu phe ala ala leu arg asp met gln trp arg lys arg arg leu
 61/21 91/31
 gtc atc acg atc atc agc acc ggg ctg atc ttc ggg atg acg ctt gtt ttg acc gga ctc
 val ile thr ile ile ser thr gly leu ile phe gly met thr leu val leu thr gly leu
 121/41 151/51
 gcg aac ggc ttc cgg gtg gag gcc cgg cac acc gtc gat tcc atg ggt gtc gat gta ttc
 ala asn gly phe arg val glu ala arg his thr val asp ser met gly val asp val phe
 181/61 211/71
 gtc gtc aga tcc ggc gct gct gga cct ttt ctg ggt tca ata ccg ttt ccc gat gtt gac
 val val arg ser gly ala ala gly pro phe leu gly ser ile pro phe pro asp val asp
 241/81 271/91
 ctg gcc cga gtg gcc gct gaa ccc ggt gtc atg gcc gcg gcc ccg ttg ggc agc gtg ggg
 leu ala arg val ala ala glu pro gly val met ala ala pro leu gly ser val gly
 301/101 331/111
 acg atc atg aaa gaa ggc acg tcg acg cga aac gtc acg gtc ttc ggc gcg ccc gag cac
 thr ile met lys glu gly thr ser thr arg asn val thr val phe gly ala pro glu his
 361/121 391/131
 gga cct ggc atg cca cgg gtc tca gag ggt cgg tca ccg tcg aaa ccg gac gaa gtc gcg
 gly pro gly met pro arg val ser glu gly arg ser pro ser lys pro asp glu val ala
 421/141 451/151
 gca tcg agc acg atg ggc cga cac ctc ggt gac act gtc gag gtc ggc gcg cgc aga ttg
 ala ser ser thr met gly arg his leu gly asp thr val glu val gly ala arg arg leu
 481/161 511/171
 cgg gtc gtt ggc att gtg ccg aat tcc acc gcg ctg gcc aag atc ccc aat gtc ttc ctc
 arg val val gly ile val pro asn ser thr ala leu ala lys ile pro asn val phe leu
 541/181 571/191
 acg acc gag ggc tta cag aaa ttg gcg tac aac ggg cag ccg aat atc acg tcc atc ggg
 thr thr glu gly leu gln lys leu ala tyr asn gly gln pro asn ile thr ser ile gly
 601/201 631/211
 atc ata ggt atg ccc cga cag ctg ccg gag ggt tac cag act ttc gat cgg gtg ggc gct
 ile ile gly met pro arg gln leu pro glu gly tyr gln thr phe asp arg val gly ala
 661/221 691/231
 gtc aat gat ttg gtg cgc cca ttg aag gtc gca gtg aat tcg atc tcg atc gtg gct gtt
 val asn asp leu val arg pro leu lys val ala val asn ser ile ser ile val ala val
 721/241 751/251
 ttg ctg tgg att gtg gcg gtg ctg atc gtc ggc tcg gtg gtg tac ctt tcg gct ctt gag
 leu leu trp ile val ala val leu ile val gly ser val val tyr leu ser ala leu glu
 781/261 811/271
 cgg cta cgt gac ttc gcg gtg ttc aag gcg att ggc acg cca acg cgc tcg att atg gcc
 arg leu arg asp phe ala val phe lys ala ile gly thr pro thr arg ser ile met ala
 841/281 871/291
 ggg ctc gca tta cag gcg ctg gtc att gcg ttg ctt gcg gcg gtg gtg ggc gtc gtc ctg
 gly leu ala leu gln ala leu val ile ala leu leu ala ala val val gly val val leu
 901/301 931/311
 gcg cag gtg ttg gca cca ctg ttt ccg atg att gtc gcg gta ccc gtc ggt gct tac ctg
 ala gln val leu ala pro leu phe pro met ile val ala val pro val gly ala tyr leu
 961/321 991/331
 gcg cta ccg gtg gcc gcg atc gtc atc ggt ctg ttc gct agt gtt gcc gga ttg aag cgc
 ala leu pro val ala ala ile val ile gly leu phe ala ser val ala gly leu lys arg
 1021/341 1051/351
 gtg gtg acg gtc gat ccc gcg cag gcg ttc gga ggt ccc tag
 val val thr val asp pro ala gln ala phe gly gly pro) AMB

SEQ ID Nos. 166-157

FIGURE 8 G

31/11
 SEQ ID No. 158 CGA GGC CGA GCG AAC CGT CGA TTC CAT GGG TGT CGA CGC ATT CGT GGT CAA GGC CGG CGC
 (arg gly arg ala asn arg arg phe his gly cys arg arg ile arg gly gln gly arg arg
 61/21 91/31
 GGC AGG ACC GTT CCT GGG TTC GAC ACC ATT CGC CCA AAT CGA CCT GCC CCA GGT TGC TCG
 gly arg thr val pro gly phe asp thr ile arg pro asn arg pro ala pro gly cys ser
 121/41 151/51
 TGC GCC TGG CGT CTT GGC TGC CGC CCC ACT AGC GAC TGC GCC GTC GAC GAT CCG GCA GGC
 cys ala trp arg leu gly cys arg pro thr ser asp cys ala val asp asp pro ala gly
 181/61 211/71
 CAC GTC AGC GCG AAA CGT CAC CGC GTT CGG GGC ACC AGA GCA CGG ACC CGG CAT GCC GCG
 his val ser ala lys arg his arg val arg gly thr arg ala arg thr arg his ala ala
 241/81 271/91
 GGT CTC GGA CGG TCG GGC GCC ATC GAC GCC GGA CGA GGT CGC GGT GTC GAG CAC GCT GGG
 gly leu gly arg ser gly ala ile asp ala gly arg gly arg gly val glu his ala gly
 301/101
 CCG AAA CCT CGG CGA CGA TC
 pro lys pro arg arg arg)

SEQ ID Nos. 158-159

FIGURE 9A

32/11
 SEQ ID No. 160 GAG GCC GAG CGA ACC GTC GAT TCC ATG GGT GTC GAC GCA TTC GTG GTC AAG GCC GGC GCG
 (glu ala glu arg thr val asp ser met gly val asp ala phe val val lys ala gly ala
 62/21 92/31
 GCA GGA CCG TTC CTG GGT TCG ACA CCA TTC GCC CAA ATC GAC CTG CCC GAG GTT GCT CGT
 ala gly pro phe leu gly ser thr pro phe ala gln ile asp leu pro gln val ala arg
 122/41 152/51
 GCG CCT GGC GTC TTG GCT GCC GCC CCA CTA GCG ACT GCG CCG TCG ACG ATC CGG CAG GGC
 ala pro gly val leu ala ala ala pro leu ala thr ala pro ser thr ile arg gln gly
 182/61 212/71
 ACG TCA GCG CGA AAC GTC ACC GCG TTC GGG GCA CCA GAG CAC GGA CCC GGC ATG CCG CGG
 thr ser ala arg asn val thr ala phe gly ala pro gly his gly pro gly met pro arg
 242/81 272/91
 GTC TCG GAC GGT CGG GCG CCA TCG ACG CCG GAC GAG GTC GCG GTG TCG AGC ACG CTG GGC
 val ser asp gly arg ala pro ser thr pro asp glu val ala val ser ser thr leu gly
 302/101
 CGA AAC CTC GGC GAC GAT C
 arg asn leu gly asp asp)

SEQ ID Nos. 160-161

FIGURE 9B

SEQ ID No. 162 → AGG CCG AGC GAA CCG TCG ATT CCA TGG GTG TCG ACG CAT TCG TGG TCA AGG CCG GCG CGG
 (arg pro ser glu pro ser ile pro trp val ser thr his ser trp ser arg pro ala arg
 63/21 93/31
 CAG GAC CGT TCC TGG GTT CGA CAC CAT TCG CCC AAA TCG ACC TGC CCC AGG TTG CTC GTG
 gln asp arg ser trp val arg his his ser pro lys ser thr cys pro arg leu leu val
 123/41 153/51
 CGC CTG GCG TCT TGG CTG CCG CCC CAC TAG CGA CTG CGC CGT CGA CGA TCC GGC AGG GCA
 arg leu ala ser trp leu pro pro his) AMB (arg leu arg arg arg arg ser gly arg ala
 183/61 213/71
 CGT CAG CGC GAA ACG TCA CCG CGT TCG GGG CAC CAG AGC ACG GAC CCG GCA TGC CGC GGG
 arg gln arg glu thr ser pro arg ser gly his gln ser thr asp pro ala cys arg gly
 243/81 273/91
 TCT CGG ACG GTC GGG CGC CAT CGA CGC CGG ACG AGG TCG CGG TGT CGA GCA CGC TGG GCC
 ser arg thr val gly arg his arg arg arg thr arg ser arg cys arg ala arg trp ala
 303/101
 GAA ACC TCG GCG ACG ATC
 glu thr. ser ala thr ile)

SEQ ID Nos. 162-164

FIGURE 9C

SEQ ID No. 165 → TTA ACG ACT CAG ACG GAA ACG CTT GAA CCG CGA GGT CGC TCC GGA CAC CAA TTT GAC TCG
 (leu thr thr gln thr glu thr leu glu pro arg gly arg ser gly his gln phe asp ser
 61/21 91/31
 GCT CTT TGG CAA TTG AAG GTG AGC TGC GAG CAG CCG GGT GAC CGC ATC GTT GGC CTT GCC
 ala leu trp gln leu lys val ser cys glu gln pro gly asp arg ile val gly leu ala
 121/41 151/51
 ATC AAT CGC CGG CTC GCG GAC GTA GAT AAT CAG CTC ACC GTT GGG ACC GAC CTC GAC CAG
 ile asn arg arg leu ala asp val asp asn gln leu thr val gly thr asp leu asp gln
 181/61 211/71
 GGG TCC TTT GTG ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA GTC GGT CAT CGC CTA AGG
 gly ser phe val thr ala gly leu asp ala asp asp his arg val gly his arg leu arg
 241/81 271/91
 CTA CCG TTC TGA CCT GGG GCT GCG TGG GCG CCG ACG ACG TGA GGC ACG TCA TGT CTC AGC
 leu pro phe) OPA (pro gly ala ala trp ala pro thr thr) OPA (gly thr ser cys leu ser
 301/101 331/111
 GGC CCA CCG CCA CCT CGG TCG CCG GCA GTA TGT CAG CAT GTG CAG ATG ACT CCA CGC AGC
 gly pro pro pro pro arg ser pro ala val cys gln his val gln met thr pro arg ser
 361/121 391/131
 CTT GTT CGC ATC GTT GGT GTC GTG GTT GCG ACG ACC TTG GCG CTG GTG AGC GCA CCC GCC
 leu val arg ile val gly val val val ala thr thr leu ala leu val ser ala pro ala
 421/141
 GGC GGT CGT GCC GCG CAT GCG GAT C
 gly gly arg ala ala his ala asp)

SEQ ID Nos. 165-168

FIGURE 10A

32/11
 TAA CGA CTC AGA CGG AAA CGC TTG AAC CGC GAG GTC GCT CCG GAC ACC AAT TTG ACT CGG
 OCH (arg leu arg arg lys arg leu asn arg glu val ala pro asp thr asn leu thr arg
 62/21
 CTC TTT GGC AAT TGA AGG TGA GCT GCG AGC AGC CGG GTG ACC GCA TCG TTG GCC TTG CCA
 leu phe gly asn) OPA arg OPA (ala ala ser ser arg val thr ala ser leu ala leu pro
 122/41
 TCA ATC GCC GGC TCG CGG ACG TAG ATA ATC AGC TCA CCG TTG GGA CCG ACC TCG ACC AGG
 ser ile ala gly ser arg thr) AMB (ile ile ser ser pro leu gly pro thr ser thr arg
 182/61
 GGT CCT TTG TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG TCG GTC ATC GCC TAA GGC
 gly pro leu) OPA (leu pro gly leu thr arg thr thr thr glu ser val ile ala) OCH (gly
 242/81
 TAC CGT TCT GAC CTG GGG CTG CGT GGG CGC CGA CGA CGT GAG GCA CGT CAT GTC TCA GCG
 tyr arg ser asp leu gly leu arg gly arg arg arg arg glu ala arg his val ser ala
 302/101
 GCC CAC CGC GAC CTC GGT CGC CGG CAG TAT GTC AGC ATG TGC AGA TGA CTC CAC GCA GCC
 ala his arg his leu gly arg arg arg gln tyr val ser met cys arg) OPA (leu his ala ala
 362/121
 TTG TTC GCA TCG TTG GTG TCG TGG TTG CGA CGA CCT TGG CGC TGG TGA GCG CAC CCG CCG
 leu phe ala ser leu val ser trp leu arg arg pro trp arg trp) OPA (ala his pro pro
 422/141
 GCG GTC GTG CCG CGC ATG CGG ATC
 ala val val pro arg met arg Ile)

SEQ ID No. 169
 SEQ ID No. 170
 SEQ ID No. 171
 SEQ ID No. 172
 SEQ ID No. 173
 SEQ ID No. 174
 SEQ ID No. 175
 SEQ ID No. 176

SEQ ID Nos. 170-176

FIGURE 10B

33/11
 AAC GAC TCA GAC GGA AAC GCT TGA ACC GCG AGG TCG CTC CGG ACA CCA ATT TGA CTC GGC
 asn asp ser asp gly asn ala) OPA (thr ala arg ser leu arg thr pro ile) OPA (leu gly
 63/21
 TCT TTG GCA ATT GAA GGT GAG CTG CGA GCA GCC GGG TGA CCG CAT CGT TGG CCT TGC CAT
 ser leu ala ile glu gly glu leu arg ala ala gly) OPA (pro his arg trp pro cys his
 123/41
 CAA TCG CCG GCT CGC GGA CGT AGA TAA TCA GCT CAC CGT TGG GAC CGA CCT CGA CCA GGG
 gln ser pro ala arg gly arg arg) OCH (ser ala his arg trp asp arg pro arg pro gly
 183/61
 GTC CTT TGT GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT CGG TCA TCG CCT AAG GCT
 val leu cys asp cys arg ala) OPA (arg gly arg pro gln ser arg ser ser pro lys ala
 243/81
 ACC GTT CTG ACC TGG GGC TGC GTG GGC GCC GAC GAC GTG AGG CAC GTC ATG TCT CAG CGG
 thr val leu thr trp gly cys val gly ala asp asp val arg his val met ser gln arg
 303/101
 CCC ACC GCC ACC TCG GTC GCC GGC AGT ATG TCA GCA TGT GCA GAT GAC TCC ACG CAG CCT
 pro thr ala thr ser val ala gly ser met ser ala cys ala asp asp ser thr gln pro
 363/121
 TGT TCG CAT CGT TGG TGT CGT GGT TGC GAC GAC CTT GGC GCT GGT GAG CGC ACC CGC CGG
 cys ser his arg trp cys arg gly cys asp asp leu gly ala gly glu arg thr arg arg
 423/141
 CGG TCG TGC CGC GCA TGC GGA TC
 arg ser cys arg ala cys gly)

SEQ ID No. 177
 SEQ ID No. 178
 SEQ ID No. 179
 SEQ ID No. 180
 SEQ ID No. 181
 SEQ ID No. 182
 SEQ ID No. 183

SEQ ID Nos. 177-183

FIGURE 10C

SEQ ID No. 184 → CCC GAA GAG GTC CCC CGT TTT GTT AAT TTT TAA AAA ATT TGT GTC ACA AAC CGG GGT ACC
 (pro glu glu val pro arg phe val asp phe) OCH (lys ile cys val thr lys arg gly thr
 61/21
 AAG GCA TAA AAC CTA GTA CCT GGG GCG GCG GAT TCA ACG AAA ACC GAG TGG GGG TAG TCA
 lys ala) OCH (asn leu val pro gly ala ala asp ser thr lys thr glu trp gly) AMB (ser
 121/41
 GGG GCG TGC ATT CCG ACG ACC CTG TAC GAC CCG CTG GTG GCA ACG CCG ATG AGT GCG CCG
 gly ala cys ile pro thr thr leu tyr asp pro leu val ala thr pro met ser ala pro
 181/61
 ACG AAG GCC GAG CGA CGG GCT GCC GGC GCT GAC CGC CGC GGA AGC CGC CGA GTG CAT GGT
 thr lys ala glu arg arg ala ala gly ala asp arg arg gly ser arg arg val asp gly
 241/81
 CAC CAC CGC CCG CAC CCG ACC GGT ACG GAT CGC GCC TCG GGT TAC CGT CGC CGT CAA CGC
 his his arg pro his pro thr gly thr asp arg ala ser gly tyr arg arg arg gln arg
 301/101
 GCT GGA CAG CAT CGG TCC CCG CTG GGT CAA TGC ACT CAT GCA GCG CCG CAA CGA ACA GCT
 ala gly gln his arg ser pro leu gly gln cys thr his ala ala pro gln arg thr ala
 361/121
 CAA CCC TTG AAC CGG GTC CCG GCC TGC CGA CCC TCG GCC GCC GGC GTG CCG CTA CGT GAT
 gln pro leu asn arg val pro ala cys arg pro ser ala ala gly val pro leu arg asp
 421/141
 AGA CAC AGG GCC ATG GAA ATC CTG GCC AGC CGG ATG CTA CTT CGG CCG GCG GAC TAT CAG
 arg his arg ala met glu ile leu ala ser arg met leu leu arg pro ala asp tyr gln
 481/161
 CGG TCG CTG AGC TTC TAC CGT GAC CAG ATC
 arg ser leu ser phe tyr arg asp gln ile)

SEQ ID Nos. 184-188

FIGURE 11A

SEQ ID No. 189 → CCG AAG AGG TCC CCC GTT TTG TTA ATT TTT AAA AAA TTT GTG TCA CAA AGC GGG GTA CCA
 (pro lys arg ser pro val leu leu ile phe lys lys phe val ser gln ser gly val pro
 62/21
 AGG CAT AAA ACC TAG TAC CTG GGG CGG CGG ATT CAA CGA AAA CCG AGT GGG GGT AGT CAG
 arg his lys thr) AMB (tyr leu gly arg arg ile gln arg lys pro ser gly gly ser gln
 122/41
 GGG CGT GCA TTC CGA CGA CCC TGT ACG ACC CGC TGG TGG CAA CGC CGA TGA GTG CCC CGA
 gly arg ala phe arg arg pro cys thr thr arg trp trp gin arg arg) OPA (val arg arg
 182/61
 CGA AGG ccG AGC GAC GGG CTG CCG GCG CTG ACC GCC GCG GAA GCC GCC GAG TGG ATG GTC
 arg arg pro ser asp gly leu pro ala leu thr ala ala glu ala ala glu trp met val
 242/81
 ACC ACC GCC CGC ACC CGA CCG GTA CGG ATC GCG CCT CGG GTT ACC GTC GCC GTC ACC GCG
 thr thr ala arg thr arg pro val arg ile ala pro arg val thr val ala val asn ala
 302/101
 CTG GAC AGC ATC GGT CCC CGC TGG GTC AAT GCA CTC ATG CAG CGC CGC AAC GAA CAG CTC
 leu asp ser ile gly pro arg trp val asn ala leu met gln arg arg asn glu gln leu
 362/121
 AAC CCT TGA ACC GGG TCC CGG CCT GCC GAC CCT CGG CCG CCG GCG TGC CGC TAC GTG ATA
 asn pro) OPA (thr gly ser arg pro ala asp pro arg pro pro ala cys arg tyr val ile
 422/141
 GAC ACA GGG CCA TGG AAA TCC TGG CCA GCC GGA TGC TAC TTC GCC CGG CGG ACT ATC AGC
 asp thr gly pro trp lys ser trp pro ala gly cys tyr phe gly arg arg thr ile ser
 482/161
 GGT CGC TGA GCT TCT ACC GTG ACC AGA TC
 gly arg) OPA (ala ser thr val thr arg)
 SEQ ID No. 194

SEQ ID Nos. 189-194

FIGURE 11B

SEQ ID No. 195 → CGA AGA GGT CCC CCG TTT TGT TAA TTT TTA AAA AAT TTG TGT CAC AAA GCG GGG TAC CAA
 (arg arg gly pro pro phe cys) OCH (phe leu lys asn leu cys his lys ala gly tyr gln
 63/21
 GGC ATA AAA CCT AGT ACC TGG GGC GGC GGA TTC AAC GAA AAC CGA GTG GGG GTA GTC AGG
 gly ile lys pro ser thr trp gly gly gly phe asn glu asn arg val gly val val arg
 123/41
 GGC GTG CAT TCC GAC GAC CCT GTA CGA CCC GCT GGT GGC AAC GCC GAT GAG TGC GCC GAC
 gly val his ser asp asp pro val arg pro ala gly gly asn ala asp glu cys ala asp
 183/61
 GAA GGC CGA GCG ACG GGC TGC CGG CGC TGA CCG CCG CGG AAG CCG CCG AGT GGA TGG TCA
 glu gly arg ala thr gly cys arg arg) OPA (pro pro arg lys pro pro ser gly trp ser
 243/81
 CCA CCG CCC GCA CCC GAC CGG TAC GGA TCG CGC CTC GGG TTA CCG TCG CCG TCA ACG CGC
 pro pro pro ala pro asp arg tyr gly ser arg leu gly leu pro ser pro ser thr arg
 303/101
 TGG ACA GCA TCG GTC CCC GCT GGG TCA ATG CAC TCA TGC AGC GCC GCA ACG AAC AGC TCA
 trp thr ala ser val pro ala gly ser met his ser cys ser ala ala thr asn ser ser
 363/121
 ACC CTT GAA CCG GGT CCC GGC CTG CCG ACC CTC GGC CGC CGG CGT GCC GCT ACG TGA TAG
 thr leu glu pro gly pro gly leu pro thr leu gly arg arg arg ala ala thr) OPA AMB
 423/141
 ACA CAG GGC CAT GGA AAT CCT GGC CAG CCG GAT GCT ACT TCG GCC GGC GGA CTA TCA GCG
 (thr gln gly his gly asn pro gly gln pro asp ala thr ser ala gly gly leu ser ala
 483/161
 GTC GCT GAG CTT CTA CCG TGA CCA GAT C
 val ala glu leu leu pro) OPA pro asp

SEQ ID Nos. 195-199

FIGURE 11C

part of the nucleotide sequence of Seq11

SEQ ID No. 200 → 1/1 31/11
 CGT CGC CGT CAA CGC GCT GGA CAG CAT CGG TCC CCG CTG GGT CAA TGC ACT CAT GCA GCG
 (arg arg arg gln arg ala gly gln his arg ser pro leu gly gln cys thr his ala ala
 61/21
 CCG CAA CGA ACA GCT CAA CCC TTG AAC CGG GTC CCG GCC TGC CGA CCC TCG GCC GCC GGC
 pro gln arg thr ala gln pro leu asn arg val pro ala cys arg pro ser ala ala gly
 121/41
 GTG CCG CTA CGT GAT AGA CAC AGG GCC ATG GAA ATC CTG GCC AGC CGG ATG CTA CTT CGG
 val pro leu arg asp arg his arg ala met glu ile leu ala ser arg met leu leu arg
 181/61
 CCG GCG GAC TAT CAG CGG TCG CTG AGC TTC TAC CGT GAC CAG ATC
 pro ala asp tyr gln arg ser leu ser phe tyr arg asp gln ile)

SEQ ID Nos 200-201

FIGURE 11A'

1/1 31/11
 SEQ ID No. 202 → GTC GCC GTC AAC GCG CTG GAC AGC ATC GGT CCC CGC TGG GTC AAT GCA CTC ATG CAG CGC
 (val ala val asn ala leu asp ser ile gly pro arg trp val asn ala leu met gln arg
 61/21 91/31
 SEQ ID No. 203 → CGC AAC GAA CAG CTC AAC CCT TGA ACC GGG TCC CGG CCT GCC GAC CCT CGG CCG CCG GCG
 arg asn glu gln leu asn pro) OPA (thr gly ser arg pro ala asp pro arg pro pro ala
 121/41 151/51
 TGC CGC TAC GTG ATA GAC ACA GGG CCA TGG AAA TCC TGG CCA GCC GGA TGC TAC TTC GGC
 cys arg tyr val ile asp thr gly pro trp lys ser trp pro ala gly cys tyr phe gly
 181/61 211/71
 CGG CGG ACT ATC AGC GGT CGC TGA GCT TCT ACC GTG ACC AGA TC
 arg arg thr ile ser gly arg) OPA (ala ser thr val thr arg)
 SEQ ID No. 205

SEQ ID Nos. 202-205

FIGURE 11B'

1/1 31/11
 SEQ ID No. 206 → TCG CCG TCA ACG CGC TGG ACA GCA TCG GTC CCC GCT GGG TCA ATG CAC TCA TGC AGC GCC
 (ser pro ser thr arg trp thr ala ser val pro ala gly ser met his ser cys ser ala
 61/21 91/31
 SEQ ID No. 207 → GCA ACG AAC AGC TCA ACC CTT GAA CCG GGT CCC GGC CTG CCG ACC CTC GGC CGC CGG CGT
 ala thr asn ser ser thr leu glu pro gly pro gly leu pro thr leu gly arg arg arg
 121/41 151/51
 GCC GCT ACG TGA TAG ACA CAG GGC CAT GGA AAT CCT GGC CAG CCG GAT GCT ACT TCG GCC
 ala ala thr) OPA (AMB thr gln gly his gly asn pro gly gln pro asp ala thr ser ala
 181/61 211/71
 GGC GGA CTA TCA GCG GTC GCT GAG CTT CTA CCG TGA CCA GAT C
 gly gly leu ser ala val ala glu leu leu pro) OPA pro asp

SEQ ID Nos. 206-208

FIGURE 11C'

sequence Rv0546c predicted by Cole et al. (Nature 393:537-544) and containing Seq11A'

1/1 31/11
 SEQ ID No. 209 → atg gaa atc ctg gcc agc cgg atg cta ctt cgg ccg gcg gac tat cag cgg tcg ctg agc
 (Met glu ile leu ala ser arg met leu leu arg pro ala asp tyr gln arg ser leu ser
 61/21 91/31
 ttc tac cgt gac cag atc ggg ctg gcg att gcc cgt gaa tac ggg gcc ggc aca gtg ttt
 phe tyr arg asp gln ile gly leu ala ile ala arg glu tyr gly ala gly thr val phe
 121/41 151/51
 ttc gcc ggt cag tca ctg ctc gaa ctg gcc ggt tac ggc gag ccg gac cat tcg cgg gga
 phe ala gly gln ser leu leu glu leu ala gly tyr gly glu pro asp his ser arg gly
 181/61 211/71
 cct ttt ccc ggc gcg ctg tgg ctg cag gtg cgc gac ctc gag gct acc cag acc gag ctg
 pro phe pro gly ala leu trp leu gln val arg asp leu glu ala thr gln thr glu leu
 241/81 271/91
 gtc agc cga ggc gtg tcg atc gct cgc gag ccc cgc cgc gaa ccg tgg ggc ctg cac gag
 val ser arg gly val ser ile ala arg glu pro arg arg glu pro trp gly leu his glu
 301/101 331/111
 atg cat gtg acc gac cca gac ggg atc aca ctg ata ttc gtc gag gtt ccc gag ggt cac
 met his val thr asp pro asp gly ile thr leu ile phe val glu val pro glu gly his
 361/121
 ccg ctg cgt aca gac acc cgg gcg tga
 pro leu arg thr asp thr arg ala) OPA

SEQ ID Nos. 209-210

FIGURE 11D

ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv0546c

1/1 31/11
 tag tca ggg cgt gca ttc gac gac gct gta cta ccc gct ggt ggc aac tcc gat gat tgc
 AMB ser gly arg ala phe asp asp ala val leu pro ala gly gly asn ser asp asp cys
 61/21 91/31
 gcc gac gaa ggc cta cga cgg gct gcc ggc gct gac cgc cgc gga agc cgc cga gtg gat
 ala asp glu gly leu arg arg ala ala gly ala asp arg arg gly ser arg arg val asp
 121/41 151/51
 ggt cac cgc cgc ccg cac ccg acc ggt gcg gat cgc gcc tcg ggt tgc cgt cgc cgt caa
 gly his arg arg pro his pro thr gly ala asp arg ala ser gly cys arg arg arg gln
 181/61 211/71
 cgc gct gga cag cat cgg tcc ccg ctg ggt caa tgc act cat gca gcg ccg caa cga aca
 arg ala gly gln his arg ser pro leu gly gln cys thr his ala ala pro gln arg thr
 241/81 271/91
 gct caa ccc ttg aac cgg gtc ccg gcc tgc cga ccc tcg gcc gcc ggc gtg ccg cta cgt
 ala gln pro leu asn arg val pro ala cys arg pro ser ala ala gly val pro leu arg
 301/101 331/111
 gat aga cac agg gcc atg gaa atc ctg gcc agc cgg atg cta ctt cgg ccg gcg gac tat
 asp arg his arg ala met glu ile leu ala ser arg met leu leu arg pro ala asp tyr
 361/121 391/131
 cag cgg tcg ctg agc ttc tac cgt gac cag atc ggg ctg gcg att gcc cgt gaa tac ggg
 gln arg ser leu ser phe tyr arg asp gln ile gly leu ala ile ala arg glu tyr gly
 421/141 451/151
 gcc ggc aca gtg ttt ttc gcc ggt cag tca ctg ctc gaa ctg gcc ggt tac ggc gag ccg
 ala gly thr val phe phe ala gly gln ser leu leu glu leu ala gly tyr gly glu pro
 481/161 511/171
 gac cat tcg cgg gga cct ttt ccc ggc gcg ctg tgg ctg cag gtg cgc gac ctc gag gct
 asp his ser arg gly pro phe pro gly ala leu trp leu gln val arg asp leu glu ala
 541/181 571/191
 acc cag acc gag ctg gtc agc cga ggc gtg tcg atc gct cgc gag ccc cgc cgc gaa ccg
 thr gln thr glu leu val ser arg gly val ser ile ala arg glu pro arg arg glu pro
 601/201 631/211
 tgg ggc ctg cac gag atg cat gtg acc gac cca gac ggg atc aca ctg ata ttc gtc gag
 trp gly leu his glu met his val thr asp pro asp gly ile thr leu ile phe val glu
 661/221 691/231
 gtt ccc gag ggt cac ccg ctg cgt aca gac acc cgg gcg tga
 val pro glu gly his pro leu arg thr asp thr arg ala)OPA

SEQ ID Nos. 211-212

FIGURE 11E

1/1 31/11
 ID No. 213 → gac cga agg gat ttc gcg act aac tcg gcc tgt aag gca acg cga ggt ctt cat gcc gag
 asp arg arg asp phe ala thr asn ser ala cys lys ala thr arg gly leu his ala glu
 61/21 91/31
 ID No. 214 → gac gta gac agg aag aga cag gga agc tga tga cgt cgc gta ccg gac cgc cat tct gtc
 asp val asp arg lys arg gln gly ser) OPA OPA (arg arg val pro asp arg his ser val
 121/41 151/51 SEQ ID No. 215
 gag tct ttc cga gtt cag caa caa tcg aca cag aag cgg gga cca gac cgg gag gac gac
 glu ser phe arg val gln gln gln ser thr gln lys arg gly pro asp arg glu asp asp
 181/61 211/71
 gcg gcc cgg gcc gct tcg ggc cga gtg tct gag taa gac cag agt cac ggg tcc gtg tgt
 ala ala arg ala ala ser gly arg val ser glu) OCH (asp gln ser his gly ser val cys
 241/81 271/91 SEQ ID No. 216
 gac aac cgc gcg gaa ttc aat cgg atg gcg ggc ggg acc gga ttg cgc cgg tca ccg agg
 asp asn arg ala glu phe asn arg met ala gly gly thr gly leu arg arg ser pro arg
 301/101
 aac ctc cgg agt gat c
 asn leu arg ser asp)

SEQ ID Nos 213-216

FIGURE 12A

1/1 31/11
 SEQ ID No. 217 → acc gaa ggg att tcg cga cta act cgg cct gta agg caa cgc gag gtc ttc atg ccg agg
 thr glu gly ile ser arg leu thr arg pro val arg gln arg glu val phe met pro arg
 61/21 91/31
 ID No. 218 → acg tag aca gga aga gac agg gaa gct gat gac gtc gcg tac cgg acc gcc att ctg tcg
 thr) AMB (thr gly arg asp arg glu ala asp asp val ala tyr arg thr ala ile leu ser
 121/41 SEQ ID No. 219 151/51
 agt ctt tcc gag ttc agc aac aat cga cac aga agc ggg gac cag acc ggg agg acg acg
 ser leu ser glu phe ser asn asn arg his arg ser gly asp gln thr gly arg thr thr
 181/61 211/71
 cgg ccc ggg ccg ctt cgg gcc gag tgt ctg agt aag acc aga gtc acg ggt ccg tgt gtg
 arg pro gly pro leu arg ala glu cys leu ser lys thr arg val thr gly pro cys val
 241/81 271/91
 aca acc gcg cgg aat tca atc gga tgg cgg gcg gga ccg gat tgc gcc ggt cac cga gga
 thr thr ala arg asn ser ile gly trp arg ala gly pro asp cys ala gly his arg gly
 301/101
 acc tcc gga gtg atc
 thr ser gly val ile)

SEQ ID Nos 217-219

FIGURE 12B

1/1

EO ID No. 220 → ccg aag gga ttt cgc gac taa ctc ggc ctg taa ggc aac gcg agg tct tca tgc cga gga
 pro lys gly phe arg asp) OCH leu gly leu OCH gly asn ala arg ser ser cys arg gly
 EO ID No. 221 61/21 91/31 SEQ ID No. 222
 cgt aga cag gaa gag aca ggg aag ctg atg acg tcg cgt acc gga ccg cca ttc tgt cga
 arg arg gln glu glu thr gly lys leu met thr ser arg thr gly pro pro phe cys arg
 121/41 151/51
 gtc ttt ccg agt tca gca aca atc gac aca gaa gcg ggg acc aga ccg gga gga cga cgc
 val phe pro ser ser ala thr ile asp thr glu ala gly thr arg pro gly gly arg arg
 181/61 211/71
 ggc ccg ggc cgc ttc ggg ccg agt gtc tga gta aga cca gag tca ccg gtc cgt gtg tga
 gly pro gly arg phe gly pro ser val) OPA (val arg pro glu ser arg val arg val) OPA
 241/81 271/91 SEQ ID No. 223
 caa ccg cgc gga att caa tcg gat ggc ggg ccg gac ccg att gcg ccg gtc acc gag gaa
 (gln pro arg gly ile gln ser asp gly gly arg asp arg ile ala pro val thr glu glu
 301/101
 EO ID No. 224 → cct ccg gag tga tc
 pro pro glu OPA)

SEQ ID Nos. 220-224

FIGURE 12C

1/1

EO ID No. 225 → GGG ATT TCG TTG CCC GAT GGA TTG TTT GTA CGG TTT GGG AAA AAC ACT TGA AGT CCT TTT
 (gly ile ser leu pro asp gly leu phe val arg phe gly lys asn thr) OPA (ser pro phe
 EO ID No. 226 → 61/21 91/31 SEQ ID No. 227
 TAT TGG CAA TGC TGG AAA TGG ACA TTC CAA TAT TGC GCG AAT TAA CCG AAC ACG GTG AGG
 tyr trp gln cys trp lys trp thr phe gln tyr cys ala asn) OCH (pro asn thr val arg
 121/41 151/51 SEQ ID No. 923
 GGG GGG CAA GCG TTT GTA CCG GGG CCA GCA AGC GCC GCC GAC CGG TTG ACC GAA GCC AGC
 gly gly gln ala phe val pro gly pro ala ser ala ala asp arg leu thr glu ala ser
 181/61 211/71
 ATG TTG TTG TGT CAG CGC GGG CTT GGT CTC GAT GTC CCG GCC TTG GCT GGA CCC GCT TCT
 met leu leu cys gln arg gly leu gly leu asp val pro ala leu ala gly pro ala ser
 241/81 271/91
 TCA AAA CAG GTT GAA CTT AAC GAC TCA AGA ACG GAA ACG CTT GAA CCG CGA CGT CGC TCC
 ser lys gln val glu leu asn asp ser arg thr glu thr leu glu pro arg arg arg ser
 301/101 331/111
 GGA CAC CAA TTT GAC TCG GCT CTT TGG CAA TTG AAG GTG AGC TGC GAG CAG CCG GGT GAC
 gly his gln phe asp ser ala leu trp gln leu lys val ser cys glu gln pro gly asp
 361/121 391/131
 CGC ATC GTT GGC CTT GCC ATC AAT CGC CGG CTC GCG GAC GTA GAT AAT CAG CTC ACC GTT
 arg ile val gly leu ala ile asn arg arg leu ala asp val asp asn gln leu thr val
 421/141 451/151
 GGG ACC GAC CTC GAC CAG GGG TCC TTT GTG ACT GCC GGG CTT GAC GCG GAC GAC CAC AGA
 gly thr asp leu asp gln gly ser phe val thr ala gly leu asp ala asp asp his arg
 481/161 511/171
 GTC GGT CAT CGC CTA AGG CTA CCG TTC TGA CCT GGG GCT GCG TGG GCG CCG ACG ACG TGA
 val gly his arg leu arg leu pro phe) OPA (pro gly ala ala trp ala pro thr thr) OPA
 541/181 571/191
 GGC ACG TCA TGT CTC AGC GGC CCA CCG CCA CCT CGG TCG CCG GCA GTA TGT CAG CAT GTG
 (gly thr ser cys leu ser gly pro pro pro pro arg ser pro ala val cys gln his val
 EO ID No. 925 → 601/201 631/211
 CAG ATG ACT CCA CGC AGC CTT GTT CGC ATC GTT GGT GTC GTG GTT GCG ACG ACC TTG GCG
 gln met thr pro arg ser leu val arg ile val gly val val val ala thr thr leu ala
 661/221 691/231
 CTG GTG AGC GCA CCC GCC GGC GGT CGT GCC GCG CAT GCG GAT C
 leu val ser ala pro ala gly gly arg ala ala his ala asp)

SEQ ID Nos. 220-221, 923-925

FIGURE 13A

32/11
 SEQ ID NO. 228 → GGA TTT CGT TGC CCG ATG GAT TGT TTG TAC GGT TTG GGA AAA ACA CTT GAA GTC CTT TTT
 (gly phe arg cys pro met asp cys leu tyr gly leu gly lys thr leu glu val leu phe
 62/21
 SEQ ID NO. 229 → ATT GGC AAT GCT GGA AAT GGA CAT TCC AAT ATT GCG CGA ATT AAC CGA ACA CGG TGA GGG
 ile gly asn ala gly asn gly his ser asn ile ala arg ile asn arg thr arg) OPA (gly
 122/41 152/51
 GGG GGC AAG CGT TTG TAC CGG GGC CAG CAA GCG CCG CCG ACC GGT TGA CCG AAG CCA GCA
 gly gly lys arg leu tyr arg gly gln gln ala pro pro thr gly) OPA (pro lys pro ala
 182/61 212/71
 TGT TGT TGT GTC AGC GCG GGC TTG GTC TCG ATG TCC CGG CCT TGG CTG GAC CCG CTT CTT
 cys cys cys val ser ala gly leu val ser met ser arg pro trp leu asp pro leu leu
 242/81 272/91
 CAA AAC AGG TTG AAC TTA ACG ACT CAA GAA CGG AAA CGC TTG AAC CGC GAC GTC GCT CCG
 gln asn arg leu asn leu thr thr gln glu arg lys arg leu asn arg asp val ala pro
 302/101 332/111
 GAC ACC AAT TTG ACT CGG CTC TTT GGC AAT TGA AGG TGA GCT GCG AGC AGC CGG GTG ACC
 asp thr asn leu thr arg leu phe gly asn) OPA arg OPA (ala ala ser ser arg val thr
 362/121 392/131
 GCA TCG TTG GCC TTG CCA TCA ATC GCC GGC TCG CGG ACG TAG ATA ATC AGC TCA CCG TTG
 ala ser leu ala leu pro ser ile ala gly ser arg thr) AMB (ile ile ser ser pro leu
 422/141 452/151
 GGA CCG ACC TCG ACC AGG GGT CCT TTG TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG
 gly pro thr ser thr arg gly pro leu) OPA (leu pro gly leu thr arg thr thr thr glu
 482/161 512/171
 TCG GTC ATC GCC TAA GGC TAC CGT TCT GAC CTG GGG CTG CGT GGG CGC CGA CGA CGT GAG
 ser val ile ala) OCH (gly tyr arg ser asp leu gly leu arg gly arg arg arg glu
 542/181 572/191
 GCA CGT CAT GTC TCA GCG GCC CAC CGC CAC CTC GGT CGC CGG CAG TAT GTC AGC ATG TGC
 ala arg his val ser ala ala his arg his leu gly arg arg gln tyr val ser met cys
 602/201 632/211
 AGA TGA CTC CAC GCA GCC TTG TTC GCA TCG TTG GTG TCG TGG TTG CGA CGA CCT TGG CGC
 arg) OPA (leu his ala ala leu phe ala ser leu val ser trp leu arg arg pro trp arg
 662/221 692/231
 TGG TGA GCG CAC CCG CCG GCG GTC GTG CCG CGC ATG CGG ATC
 trp) OPA (ala his pro pro ala val val pro arg met arg ile)
 SEQ ID NO. 237

SEQ ID NOS. 228-237

FIGURE 13B

33/11
 SEQ ID NO. 238 GAT TTC GTT GCC CGA TGG ATT GTT TGT ACG GTT TGG GAA AAA CAC TTG AAG TCC TTT TTA
 (asp phe val ala arg trp ile val cys thr val trp glu lys his leu lys ser phe leu
 63/21 93/31
 SEQ ID NO. 239 TTG GCA ATG CTG GAA ATG GAC ATT CCA ATA TTG CGC GAA TTA ACC GAA CAC GGT GAG GGG
 leu ala met leu glu met asp ile pro ile leu arg glu leu thr glu his gly glu gly
 123/41 153/51
 GGG GCA AGC GTT TGT ACC GGG GCC AGC AAG CGC CGC CGA CCG GTT GAC CGA AGC CAG CAT
 gly ala ser val cys thr gly ala ser lys arg arg arg pro val asp arg ser gln his
 183/61 213/71
 GTT GTT GTG TCA GCG CGG GCT TGG TCT CGA TGT CCC GGC CTT GGC TGG ACC CGC TTC TTC
 val val val ser ala arg ala trp ser arg cys pro gly leu gly trp thr arg phe phe
 243/81 273/91
 AAA ACA GGT TGA ACT TAA CGA CTC AAG AAC GGA AAC GCT TGA ACC GCG ACG TCG CTC CGG
 lys thr gly) OPA thr OCH (arg leu lys asn gly asn ala) OPA (thr ala thr ser leu arg
 303/101 333/111
 ACA CCA ATT TGA CTC GGC TCT TTG GCA ATT GAA GGT GAG CTG CGA GCA GCC GGG TGA CCG
 thr pro ile) OPA (leu gly ser leu ala ile glu gly glu leu arg ala ala gly) OPA (pro
 363/121 393/131
 CAT CGT TGG CCT TGC CAT CAA TCG CCG GCT CGC GGA CGT AGA TAA TCA GCT CAC CGT TGG
 his arg trp pro cys his gln ser pro ala arg gly arg arg) OCH (ser ala his arg trp
 423/141 453/151
 GAC CGA CCT CGA CCA GGG GTC CTT TGT GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT
 asp arg pro arg pro gly val leu cys asp cys arg ala) OPA (arg gly arg pro gln ser
 483/161 513/171
 CGG TCA TCG CCT AAG GCT ACC GTT CTG ACC TGG GGC TGC GTG GGC GCC GAC GAC GTG AGG
 arg ser ser pro lys ala thr val leu thr trp gly cys val gly ala asp asp val arg
 543/181 573/191
 CAC GTC ATG TCT CAG CGG CCC ACC GCC ACC TCG GTC GCC GGC AGT ATG TCA GCA TGT GCA
 his val met ser gln arg pro thr ala thr ser val ala gly ser met ser ala cys ala
 603/201 633/211
 GAT GAC TCC ACG CAG CCT TGT TCG CAT CGT TGG TGT CGT GGT TGC GAC GAC CTT GGC GCT
 asp asp ser thr gln pro cys ser his arg trp cys arg gly cys asp asp leu gly ala
 663/221 693/231
 GGT GAG CGC ACC CGC CGG CGG TCG TGC CGC GCA TGC GGA TC
 gly glu arg thr arg arg arg ser cys arg ala cys gly)

SEQ ID Nos. 238-245

FIGURE 13C

part of the nucleotide sequence of seq13A

1/1 31/11
 10 ID No. 246 → GGG TCC TTT GTG ACT GCC GGG CTT GAC GCG GAC CAC AGA GTC GGT CAT CGC CTA AGG
 (gly ser phe val thr ala gly leu asp ala asp asp his arg val gly his arg leu arg
 10 ID No. 247 → 61/21 91/31
 CTA CCG TTC TGA CCT GGG GCT GCG TGG GCG CCG ACG ACG TGA GGC ACG TCA TGT CTC AGC
 leu pro phe) OPA (pro gly ala ala trp ala pro thr thr) OPA (gly thr ser cys leu ser
 121/41 151/51
 GGC CCA CCG CCA CCT CGG TCG CCG GCA GTA TGT CAG CAT GTG CAG ATG ACT CCA CGC AGC
 gly pro pro pro pro arg ser pro ala val cys gln his val gln met thr pro arg ser
 181/61 211/71
 CTT GTT CGC ATC GTT GGT GTC GTG GTT GCG ACG ACC TTG GCG CTG GTG AGC GCA CCC GCC
 leu val arg ile val gly val val val ala thr thr leu ala leu val ser ala pro ala
 241/81
 GGC GGT CGT GCC GCG CAT GCG GAT C
 gly gly arg ala ala his ala asp)

SEQ ID Nos. 246-249

FIGURE 13A'

1/1 31/11
 10 ID No. 250 → GGT CCT TTG TGA CTG CCG GGC TTG ACG CGG ACG ACC ACA GAG TCG GTC ATC GCC TAA GGC
 gly pro (leu OPA leu pro gly leu thr arg thr thr thr glu ser val ile ala) OCH (gly
 61/21 91/31
 TAC CGT TCT GAC CTG GGG CTG CGT GGG CGC CGA CGA CGT GAG GCA CGT CAT GTC TCA GCG
 tyr arg ser asp leu gly leu arg gly arg arg arg arg glu ala arg his val ser ala
 121/41 151/51
 GCC CAC CGC CAC CTC GGT CGC CGG CAG TAT GTC AGC ATG TGC AGA TGA CTC CAC GCA GCC
 ala his arg his leu gly arg arg gln tyr val ser met cys arg) OPA (leu his ala ala
 181/61 211/71
 TTG TTC GCA TCG TTG GTG TCG TGG TTG CGA CGA CCT TGG CGC TGG TGA GCG CAC CCG CCG
 leu phe ala ser leu val ser trp leu arg arg pro trp arg trp) OPA (ala his pro pro
 241/81
 GCG GTC GTG CCG CGC ATG CGG ATC
 ala val val pro arg met arg ile)

SEQ ID Nos. 250-254

FIGURE 13B'

1/1 31/11
 10 ID No. 255 → GTC CTT TGT GAC TGC CGG GCT TGA CGC GGA CGA CCA CAG AGT CGG TCA TCG CCT AAG GCT
 (val leu cys asp cys arg ala) OPA (arg gly arg pro gln ser arg ser ser pro lys ala
 10 ID No. 256 → 61/21 91/31
 ACC GTT CTG ACC TGG GGC TGC GTG GGC GGC GAC GAC GTG AGG CAC GTC ATG TCT CAG CGG
 thr val leu thr trp gly cys val gly ala asp asp val arg his val met ser gln arg
 121/41 151/51
 CCC ACC GCC ACC TCG GTC GCC GGC AGT ATG TCA GCA TGT GCA GAT GAC TCC ACG CAG CCT
 pro thr ala thr ser val ala gly ser met ser ala cys ala asp asp ser thr gln pro
 181/61 211/71
 TGT TCG CAT CGT TGG TGT CGT GGT TGC GAC GAC CTT GGC GCT GGT GAG CGC ACC CGC CGG
 cys ser his arg trp cys arg gly cys asp asp leu gly ala gly glu arg thr arg arg
 241/81
 CGG TCG TGC CGC GCA TGC GGA TC
 arg ser cys arg ala cys gly)

SEQ ID Nos. 255-257

FIGURE 13C'

sequence Rv1984c predicted by Cole et al. (Nature 393:537-544) and containing seq13A'

1/1

31/11

EW ID No. 258
IS ID No. 259

atg act cca cgc agc ctt gtt cgc atc gtt	ggt gtc gtg gtt gcg acg acc ttg gcg ctg
(Met thr pro arg ser leu val arg ile val	gly val val val ala thr thr leu ala leu
61/21	91/31
gtg agc gca ccc gcc ggc ggt cgt gcc gcg	cat gcg gat ccg tgt tcg gac atc gcg gtc
val ser ala pro ala gly gly arg ala ala	his ala asp pro cys ser asp ile ala val
121/41	151/51
gtt ttc gct cgc ggc acg cat cag gct tct	ggt ctt ggc gac gtc ggt gag gcg ttc gtc
val phe ala arg gly thr his gln ala ser	gly leu gly asp val gly glu ala phe val
181/61	211/71
gac tcg ctt acc tcg caa gtt ggc ggc cgg	tcg att ggg gtc tac gcg gtg aac tac cca
asp ser leu thr ser gln val gly gly arg	ser ile gly val tyr ala val asn tyr pro
241/81	271/91
gca agc gac gac tac cgc gcg agc gcg tca	aac ggt tcc gat gat gcg agc gcc cac atc
ala ser asp asp tyr arg ala ser ala ser	asn gly ser asp asp ala ser ala his ile
301/101	331/111
cag cgc acc gtc gcc agc tgc ccg aac acc	agg att gtg ctt ggt ggc tat tcg cag ggt
gln arg thr val ala ser cys pro asn thr	arg ile val leu gly gly tyr ser gln gly
361/121	391/131
gcg acg gtc atc gat ttg tcc acc tcg gcg	atg ccg ccc gcg gtg gca gat cat gtc gcc
ala thr val ile asp leu ser thr ser ala	met pro pro ala val ala asp his val ala
421/141	451/151
gct gtc gcc ctt ttc ggc gag cca tcc agt	ggt ttc tcc agc atg ttg tgg ggc ggc ggg
ala val ala leu phe gly glu pro ser ser	gly phe ser ser met leu trp gly gly gly
481/161	511/171
tcg ttg ccg aca atc ggt ccg ctg tat agc	tct aag acc ata aac ttg tgt gct ccc gac
ser leu pro thr ile gly pro leu tyr ser	ser lys thr ile asn leu cys ala pro asp
541/181	571/191
gat cca ata tgc acc gga ggc ggc aat att	atg gcg cat gtt tcg tat gtt cag tcg ggg
asp pro ile cys thr gly gly gly asn ile	met ala his val ser tyr val gln ser gly
601/201	631/211
atg aca agc cag gcg gcg aca ttc gcg gcg	aac agg ctc gat cac gcc gga tga
met thr ser gln ala ala thr phe ala ala	asn arg leu asp his ala gly) OPA

SEQ ID Nos. 258-259

FIGURE 13D

Seq13F: ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv1984c

1/1

31/11

20 ID No. 260 *tga ggc acg tca tgt ctc agc ggc cca ccg cca cct cgg tcg ccg gca gta tgt cag cat
 OPA gly thr ser cys leu ser gly pro pro pro pro arg ser pro ala val cys gln his
 20 ID No. 261 61/21 91/31
 gtg cag atg act cca cgc agc ctt gtt cgc atc gtt ggt gtc gtg gtt gcg acg acc ttg
 val gln met thr pro arg ser leu val arg ile val gly val val ala thr thr leu
 121/41 151/51
 gcg ctg gtg agc gca ccc gcc ggc ggt cgt gcc gcg cat gcg gat ccg tgt tcg gac atc
 ala leu val ser ala pro ala gly gly arg ala ala his ala asp pro cys ser asp ile
 181/61 211/71
 gcg gtc gtt ttc gct cgc ggc acg cat cag gct tct ggt ctt ggc gac gtc ggt gag gcg
 ala val val phe ala arg gly thr his gln ala ser gly leu gly asp val gly glu ala
 241/81 271/91
 ttc gtc gac tcg ctt acc tcg caa gtt ggc ggg cgg tcg att ggg gtc tac gcg gtg aac
 phe val asp ser leu thr ser gln val gly gly arg ser ile gly val tyr ala val asn
 301/101 331/111
 tac cca gca agc gac gac tac cgc gcg agc gcg tca aac ggt tcc gat gat gcg agc gcc
 tyr pro ala ser asp asp tyr arg ala ser ala ser asn gly ser asp asp ala ser ala
 361/121 391/131
 cac atc cag cgc acc gtc gcc agc tgc ccg aac acc agg att gtg ctt ggt ggc tat tcg
 his ile gln arg thr val ala ser cys pro asn thr arg ile val leu gly gly tyr ser
 421/141 451/151
 cag ggt gcg acg gtc atc gat ttg tcc acc tcg gcg atg ccg ccc gcg gtg gca gat cat
 gln gly ala thr val ile asp leu ser thr ser ala met pro pro ala val ala asp his
 481/161 511/171
 gtc gcc gct gtc gcc ctt ttc ggc gag cca tcc agt ggt ttc tcc agc atg ttg tgg gcc
 val ala ala val ala leu phe gly glu pro ser ser gly phe ser ser met leu trp gly
 541/181 571/191
 ggc ggg tcg ttg ccg aca atc ggt ccg ctg tat agc tct aag acc ata aac ttg tgt gct
 gly gly ser leu pro thr ile gly pro leu tyr ser ser lys thr ile asn leu cys ala
 601/201 631/211
 ccc gac gat cca ata tgc acc gga ggc ggc aat att atg gcg cat gtt tcg tat gtt cag
 pro asp asp pro ile cys thr gly gly gly asn ile met ala his val ser tyr val gln
 661/221 691/231
 tcg ggg atg aca agc cag gcg gcg aca ttc gcg gcg aac agg ctc gat cac gcc gga tga
 ser gly met thr ser gln ala ala thr phe ala ala asn arg leu asp his ala gly) OPA

SEQ ID Nos. 260-261

FIGURE 13F

ID No. 262 31/11
 CCA CCG GGG CTG GAG GGG CGA ATG TGC GCC GAA CGC CGT CGG CCA ACT TGG CCG CTG AGG
 ID No. 263 (pro pro gly leu glu gly arg met cys ala glu arg arg arg pro thr trp pro leu arg
 61/21 91/31
 GCG GCT GAT CCC CTG GCC CGA GAC GGG GCA AGC CAA TAG CGG CTC CAT CGG GCT TTG CTG
 ala ala asp pro leu ala arg asp gly ala ser gln)AMB (arg leu his arg ala leu leu
 121/41 151/51 SEQ ID No. 264
 GTA GCG GTT CGG CGG GAA CCG AGC GCC GAC GTT GTC GGT GCC CGG TGA TAT ATT GGG TCA
 val ala val arg arg glu pro ser ala asp val val gly ala arg)OPA (tyr ile gly ser
 181/61 211/71 SEQ ID No. 265
 GAC GGG TAT GGC GGC GAC TGA GGT GAT CTG CGA CAC GCC GCC GCG GTG CTC GAG CCA GGC
 asp gly tyr gly gly asp)OPA (gly asp leu arg his ala ala ala val leu glu pro gly
 241/81 271/91
 TTA CGA CCA GGG AAT TTC GAA AAT GTT ATT CAG AAC ATC TTG TAT CTC TTC CTC CGT GCC
 leu arg pro gly asn phe glu asn val ile gln asn ile leu tyr leu phe leu arg ala
 301/101 331/111
 ACC CCC TAG GTG TAG TGT TTT CGA GTA CCG GCA GAT CCC AGT TCA CCA GTC TCA CCA GAT
 thr pro)AMB val AMB (cys phe arg val pro ala asp pro ser ser pro val ser pro asp)
 SEQ ID No 267

C

SEQ ID Nos. 262-267

FIGURE 14A

ID No 268 32/11
 CAC CGG GGC TGG AGG GGC GAA TGT GCG CCG AAC GCC GTC GGC CAA CTT GGC CGC TGA GGG
 ID No 269 (his arg gly trp arg gly glu cys ala pro asn ala val gly gln leu gly arg)OPA (gly
 62/21 92/31 SEQ ID No. 270
 CGG CTG ATC CCC TGG CCC GAG ACG GGG CAA GCC AAT AGC GGC TCC ATC GGG CTT TGC TGG
 arg leu ile pro trp pro glu thr gly gln ala asn ser gly ser ile gly leu cys trp)
 122/41 152/51
 TAG CGG TTC GGC GGC AAC CGA GCG CCG ACG TTG TCG GTG CCC GGT GAT ATA TTG GGT CAG
 AMB (arg phe gly gly asn arg ala pro thr leu ser val pro gly asp ile leu gly gln
 SEQ ID No. 271 182/61 212/71
 ACG GGT ATG GCG GCG ACT GAG GTG ATC TGC GAC ACG CCG CCG CGG TGC TCG AGC CAG GCT
 thr gly met ala ala thr glu val ile cys asp thr pro pro arg cys ser ser gln ala
 242/81 272/91
 TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC AGA ACA TCT TGT ATC TCT TCC TCC GTG CCA
 tyr asp gln gly ile ser lys met leu phe arg thr ser cys ile ser ser ser val pro
 302/101 332/111
 CCC CCT AGG TGT AGT GTT TTC GAG TAC CGG CAG ATC CCA GTT CAC CAG TCT CAC CAG ATC
 pro pro arg cys ser val phe glu tyr arg gln ile pro val his gln ser his gln ile)

SEQ ID Nos. 268-271

FIGURE 14B

33/11
 SEQ ID NO. 274 ACC GGG GCT GGA GGG GCG AAT GTG CGC CGA ACG CCG TCG GCC AAC TTG GCC GCT GAG GGC
 (thr gly ala gly gly ala asn val arg arg thr pro ser ala asn leu ala ala glu gly
 63/21
 SEQ ID NO. 275 GGC TGA TCC CCT GGC CCG AGA CGG GGC AAG CCA ATA GCG GCT CCA TCG GGC TTT GCT GGT
 gly) OPA (ser pro gly pro arg arg gly lys pro ile ala ala pro ser gly phe ala gly
 123/41
 SEQ ID NO. 276 AGC GGT TCG GCG GGA ACC GAG CGC CGA CGT TGT CGG TGC CCG GTG ATA TAT TGG GTC AGA
 ser gly ser ala gly thr glu arg arg arg cys arg cys pro val ile tyr trp val arg
 183/61
 CGG GTA TGG CGG CGA CTG AGG TGA TCT GCG ACA CGC CGC CGC GGT GCT CGA GCC AGG CTT
 arg val trp arg arg leu arg) OPA (ser ala thr arg arg arg gly ala arg ala arg leu
 243/81
 SEQ ID NO. 277 ACG ACC AGG GAA TTT CGA AAA TGT TAT TCA GAA CAT CTT GTA TCT CTT CCT CCG TGC CAC
 thr thr arg glu phe arg lys cys tyr ser glu his leu val ser leu pro pro cys his
 303/101
 333/111
 CCC CTA GGT GTA GTG TTT TCG AGT ACC GGC AGA TCC CAG TTC ACC AGT CTC ACC AGA TC
 pro leu gly val val phe ser ser thr gly arg ser gln phe thr ser leu thr arg)

SEQ ID NOS. 274-277

FIGURE 14C

part of the nucleotide sequence of seq14A

1/1
 31/11
 SEQ ID NO. 278 TTT TCG AGT ACC GGC AGA TCC CAG GTT CAC CAG GTC TCA CCA GAT C
 1/1
 SEQ ID NO. 279 phe ser ser thr gly arg ser gln val his gln val ser pro asp

SEQ ID NOS. 278-279

FIGURE 14A'

1/1
 31/11
 SEQ ID NO. 280 TGT TTT CGA GTA CCG GCA GAT CCC AGG TTC ACC AGG TCT CAC CAG ATC
 1/1
 SEQ ID NO. 281 cys phe arg val pro ala asp pro arg phe thr arg ser his gln ile

SEQ ID NOS. 280-281

FIGURE 14C

1/1
 31/11
 SEQ ID NO. 282 GTT TTC GAG TAC CGG CAG ATC CCA GGT TCA CCA GGT CTC ACC AGA TC
 1/1
 SEQ ID NO. 283 val phe glu tyr arg gln ile pro gly ser pro gly leu thr arg

SEQ ID NOS. 282-283

FIGURE 14C'

ORF predicted based on the sequence published by Cole et al. (Nature 393:537-544) and containing seq14A'

1/1	31/11
SEQ ID NO. 284	AMB
61/21	91/31
121/41	151/51
181/61	211/71
241/81	271/91
301/101	331/111
361/121	391/131
421/141	

TAG CGG TTC GGC GGG AAG CTA GCG GCG ACG TTG TCG GTG GCC GGT GAT ATA TTG GGT CAG
 arg phe gly gly lys leu ala ala thr leu ser val ala gly asp ile leu gly gln
 ACG GGT ATG GCG GCG GCT GAG GTG ATC TGC GAC ACG CCG CCG CGG TGC TCG AGC CAG GCT
 thr gly met ala ala ala glu val ile cys asp thr pro pro arg cys ser ser gln ala
 TAC GAC CAG GGA ATT TCG AAA ATG TTA TTC AGA ACA TCT TGT ATC TCT TCT CCG TGC CAC
 tyr asp gln gly ile ser lys met leu phe arg thr ser cys ile ser ser pro cys his
 CCC CTA GGT GTA GTG TTT TCG AGT ACC GGC AGA TCC CAG GTT CAC CAG GTC TCA CCA gat
 pro leu gly val val phe ser ser thr gly arg ser gln val his gln val ser pro asp
 cca cgg ggc gcg atg aac ttc ccg gca tcg gca tcg cca ggt cga cgg acg tgg tcg cgc
 pro arg gly ala met asn phe pro ala ser ala ser pro gly arg arg thr trp ser arg
 tat gac ggg aat ctg gag cct tgt cgg gcc gct caa cat atc gaa gat gca cta ctt gag
 tyr asp gly asn leu glu pro cys arg ala ala gln his ile glu asp ala leu leu glu
 tcg ttg cca gat cct gtc aga ttc ccg att tcc gca aag gag cgg tac gcc cat gac cgt
 ser leu pro asp pro val arg phe pro ile ser ala lys glu arg tyr ala his asp arg
 gac cgt tta cac taa
 asp arg leu his) OCH

SEQ ID Nos. 284-285

FIGURE 14D

Sequence Rv3054c predicted by Cole et al. (Nature 393:537-544)
which may be in phase with Seq14A'

1/1	31/11
gtg tca gat acc aag tcc gac atc aaa atc	ttg gcc tta gtg gga agc ctg cgc gcg gcg
(val ser asp thr lys ser asp ile lys ile	leu ala leu val gly ser leu arg ala ala
61/21	91/31
tcg ttc aac cgc cag atc gcc gag ctg gct	gcc aag gtc gct ccg gac ggc gtc acc gtc
ser phe asn arg gln ile ala glu leu ala	ala lys val ala pro asp gly val thr val
121/41	151/51
acc atg ttc gag ggg ctg ggg gac ctg ccg	ttc tac aac gaa gac atc gac aca gcg acg
thr met phe glu gly leu gly asp leu pro	phe tyr asn glu asp ile asp thr ala thr
181/61	211/71
gag gtg ccg gcg ccg gtg agc gcg ttg cgg	gag gcc gcg tct gac gcg cac gct gcc ttg
glu val pro ala pro val ser ala leu arg	glu ala ala ser asp ala his ala ala leu
241/81	271/91
gtg gtc acg ccg gaa tac aac ggc agc att	ccg gcc gtg atc aag aac gcg atc gac tgg
val val thr pro glu tyr asn gly ser ile	pro ala val ile lys asn ala ile asp trp
301/101	331/111
ctg tcc agg cca ttc ggc gat ggc gcg ttg	aag gac aag ccg ttg gcc gtg atc ggc ggc
leu ser arg pro phe gly asp gly ala leu	lys asp lys pro leu ala val ile gly gly
361/121	391/131
tcc atg ggc cgc tac ggc ggg gta tgg gcg	cac gac gag act cgc aag tcg ttc agc atc
ser met gly arg tyr gly gly val trp ala	his asp glu thr arg lys ser phe ser ile
421/141	451/151
gct ggc acg ccg gtg gtc gat gcg atc aaa	ctg tcg gtg ccg ttc caa act ctg ggc aag
ala gly thr arg val val asp ala ile lys	leu ser val pro phe gln thr leu gly lys
481/161	511/171
tcg gtc gcg gac gac gcc ggg ctg gcg gcg	aat gtg cgc gac gcc gtc ggc aac ttg gcc
ser val ala asp asp ala gly leu ala ala	asn val arg asp ala val gly asn leu ala
541/181	
gct gag gtc ggc tga	
ala glu val gly) OPA	

SEQ ID Nos. 286-287

FIGURE 14E

ORF predicted by Cole et al. (Nature 393:537-544) and containing Rv3054c

1/1

31/11

SD ID No. 288

taa cgc gat cgg aat aaa tcg gac cat ggt ccg gtt ggc tcg tgc aag gac gtg gac caa
OCH arg asp arg asn lys ser asp his gly pro val gly ser cys lys asp val asp gln

SD ID No. 289

61/21 91/31

caa gcg gaa agg aac gta gca gtg tca gat acc aag tcc gac atc aaa atc ttg gcc tta
gln ala glu arg asn val ala val ser asp thr lys ser asp ile lys ile leu ala leu
121/41 151/51

gtg gga agc ctg cgc gcg gcg tcg ttc aac cgc cag atc gcc gag ctg gct gcc aag gtc
val gly ser leu arg ala ala ser phe asn arg gln ile ala glu leu ala ala lys val
181/61 211/71

gct ccg gac ggc gtc acc gtc acc atg ttc gag ggg ctg ggg gac ctg ccg ttc tac aac
ala pro asp gly val thr val thr met phe glu gly leu gly asp leu pro phe tyr asn
241/81 271/91

gaa gac atc gac aca gcg acg gag gtg ccg gcg ccg gtg agc gcg ttg ccg gag gcc gcg
glu asp ile asp thr ala thr glu val pro ala pro val ser ala leu arg glu ala ala
301/101 331/111

tct gac gcg cac gct gcc ttg gtg gtc acg ccg gaa tac aac ggc agc att ccg gcc gtg
ser asp ala his ala ala leu val val thr pro glu tyr asn gly ser ile pro ala val
361/121 391/131

atc aag aac gcg atc gac tgg ctg tcc agg cca ttc ggc gat ggc gcg ttg aag gac aag
ile lys asn ala ile asp trp leu ser arg pro phe gly asp gly ala leu lys asp lys
421/141 451/151

ccg ttg gcc gtg atc ggc ggc tcc atg ggc ccg tac ggc ggg gta tgg gcg cac gac gag
pro leu ala val ile gly gly ser met gly arg tyr gly gly val trp ala his asp glu
481/161 511/171

act cgc aag tcg ttc agc atc gct ggc acg ccg gtg gtc gat gcg atc aaa ctg tcg gtg
thr arg lys ser phe ser ile ala gly thr arg val val asp ala ile lys leu ser val
541/181 571/191

ccg ttc caa act ctg ggc aag tcg gtc gcg gac gac gcc ggg ctg gcg gcg aat gtg cgc
pro phe gln thr leu gly lys ser val ala asp asp ala gly leu ala ala asn val arg
601/201 631/211

gac gcc gtc ggc aac ttg gcc gct gag gtc ggc tga
asp ala val gly asn leu ala ala glu val gly) OPA

SEQ ID Nos. 288-289

FIGURE 14F

fragment based on the sequence published by Cole et al. (Nature 393:537-544) and containing seq 14F' and seq 14P'

SEQ ID NO. 297

SEQ ID NO. 310

31/11

caa cgc gat cgg aat aaa tcg gac cat ggt ccg gtt ggc tcg tgc aag gac gtg gac caa
OCH arg asp arg asn lys ser asp his gly pro val gly ser cys lys asp val asp gln

asn ala ile gly ile asn arg thr met val arg leu ala arg ala arg thr trp thr asn

(thr arg ser glu) OCH (ile gly pro trp ser gly trp leu val gln gly arg gly pro thr

61/21

SEQ ID NO. 312

91/31

caa cgc gaa agg aac gta gca gtg tca gat acc aag tcc gac atc aaa atc ttg gcc tta
gln ala glu arg asn val ala val ser asp thr lys ser asp ile lys ile leu ala leu

lys arg lys gly thr) AMB (gln cys gln ile pro ser pro thr ser lys ser trp pro) AMB

ser gly lys glu arg ser ser val arg tyr gln val arg his gln asn leu gly leu ser

121/41

SEQ ID NO. 299

151/51

gtg gga agc ctg cgc gcg gcg tcg ttc aac cgc cag atc gcc gag ctg gct gcc aag gtc
val gly ser leu arg ala ala ser phe asn arg gln ile ala glu leu ala ala lys val

(trp glu ala cys ala arg arg arg ser arg gly trp gly thr cys arg ser thr thr

gly lys pro ala arg gly val val gln pro pro asp arg arg ala gly cys gln gly arg

181/61

211/71

gct ccg gac ggc gtc acc gtc acc atg ttc gag ggg ctg ggg gac ctg ccg ttc tac aac
ala pro asp gly val thr val thr met phe glu gly leu gly asp leu pro phe tyr asn

leu arg thr ala ser pro ser pro cys ser arg gly trp gly thr cys arg ser thr thr

ser gly arg arg his arg his his val arg gly ala gly gly pro ala val leu gln arg

241/81

271/91

gaa gac atc gac aca gcg acg gag gtg ccg gcg ccg gtg agc gcg ttg ccg gag gcc gcg
glu asp ile asp thr ala thr glu val pro ala pro val ser ala leu arg glu ala ala

lys thr ser thr gln arg arg arg cys arg arg) OPA (ala arg cys gly arg pro arg)

arg his arg his ser asp gly gly ala gly ala gly glu arg val ala gly gly arg val

301/101

331/111

SEQ ID NO. 301

tct gac gcg cac gct gcc ttg gtg gtc acg ccg gaa tac aac gcc agc att ccg gcc gtg

ser asp ala his ala ala leu val val thr pro glu tyr asn gly ser ile pro ala val

leu thr arg thr leu pro trp trp ser arg arg asn thr thr ala ala phe arg pro OPA

OPA (arg ala arg cys leu gly gly his ala gly ile gln arg gln his ser gly arg asp

361/121

391/131

atc aag aac gcg atc gac tgg ctg tcc agg cca ttc gcc gat gcc gcg ttg aag gac aag

ile lys asn ala ile asp trp leu ser arg pro phe gly asp gly ala leu lys asp lys

(ser arg thr arg ser thr gly cys pro gly his ser ala met ala arg) OPA (arg thr ser

gln glu arg asp arg leu ala val gln ala ile arg arg trp arg val glu gly gln ala

421/141

451/151

ccg ttg gcc gtg atc gcc gcc tcc atg gcc cgc tac gcc ggg gta tgg gcg cac gac gag

pro leu ala val ile gly gly ser met gly arg tyr gly gly val trp ala his asp glu

arg trp pro) OPA (ser ala ala pro trp ala ala thr ala gly tyr gly arg thr thr arg

val gly arg asp arg arg leu his gly pro leu arg arg gly met gly ala arg arg asp

481/161

SEQ ID NO. 304

511/171

act cgc aag tcg ttc agc atc gct gcc acg ccg gtg gtc gat gcg atc aaa ctg tcg gtg

thr arg lys ser phe ser ile ala gly thr arg val val asp ala ile lys leu ser val

leu ala ser arg ser ala ser leu ala arg gly trp ser met arg ser asn cys arg cys

ser gln val val gln his arg trp his ala gly gly arg cys asp gln thr val gly ala

541/181

571/191

ccg ttc caa act ctg gcc aag tcg gtc gcg gac gac gcc ggg ctg gcg gcg aat gtg cgc

pro phe gln thr leu gly lys ser val ala asp asp ala gly leu ala ala asn val arg

arg ser lys leu trp ala ser arg ser arg thr thr pro gly trp arg arg met cys ala

val pro asn ser gly gln val gly arg gly arg ala gly gly glu cys ala arg

601/201

631/211

SEQ ID NO. 292

gac gcc gtc gcc aac ttg gcc gct gag gtc gcc tga tcc ctg gcc cga gcc ggg tca gcc

asp ala val gly asn leu ala ala glu val gly) OPA (ser leu gly arg gly gly ser ala

thr pro ser ala thr trp pro leu arg ser ala asp pro trp ala glu ala gly gln pro

arg arg arg gln leu gly arg) OPA (gly arg leu ile pro gly pro arg arg val ser gln)

661/221

SEQ ID NO. 314

691/231

SEQ ID NO. 293

aat agc gcc tcc atc gcc ttt gct ggt agc ggt tcg gcg gga agc tag (ccg cga cgt tgt

asn ser gly ser ile gly phe ala gly ser gly ser ala gly ser) AMB (arg arg arg cys

ile ala ala pro ser ala leu leu val ala val arg arg glu ala ser gly asp val val

AMB (arg leu his arg leu cys trp) AMB (arg phe gly gly lys leu ala ala thr leu ser

SEQ ID NO. 315

SEQ ID NO. 316

SEQ ID NOS. 290-316

721/241 751/251 ~~SEQ ID No. 294~~
 cgg tgg ccg gtg ata tat tgg gtc aga cgg gta tgg cgg cgg ctg agg tga tct gcg aca
 arg trp pro val ile tyr trp val arg arg val trp arg arg leu arg) OPA (ser ala thr
 gly gly arg) OPA (tyr ile gly ser asp gly tyr gly gly gly OPA (gly asp leu arg his
 val ala gly asp ile leu gly gln thr gly met ala ala ala glu val ile cys asp thr
 781/261 ~~SEQ ID No. 305~~ 811/271 ~~SEQ ID No. 304~~
 cgc cgc cgc ggt gct cga gcc agg ctt acg acc agg gaa ttt cga aaa tgt tat tca gaa
 arg arg arg gly ala arg ala arg leu thr thr arg glu phe arg lys cys tyr ser glu
 ala ala ala val leu glu pro gly leu arg pro gly asn phe glu asn val ile gln asn
 pro pro arg cys ser ser gln ala tyr asp gln gly ile ser lys met leu phe arg thr
 841/281 871/291 ~~SEQ ID No. 295~~
 cat ctt gta tct ctt ctc cgt gcc acc ccc tag gtg tag tgt ttt cga gta ccg gca gat
 his leu val ser leu leu arg ala thr pro) AMB val AMB (cys phe arg val pro ala asp
 ile leu tyr leu phe ser val pro pro pro arg cys ser val phe glu tyr arg gln ile
 ser cys ile ser ser pro cys his pro leu gly val val phe ser ser thr gly arg ser
 901/301 931/311 ~~SEQ ID No. 296~~
 ccc agg ttc acc agg tct cac cag atc cac ggg cgc cga tga act tcc cgg cat cgg cat
 pro arg phe thr arg ser his gln ile his gly ala arg) OPA (thr ser arg his arg his
 pro gly ser pro gly leu thr arg ser thr gly arg asp glu leu pro gly ile gly ile
 gln val his gln val ser pro asp pro arg gly ala met asn phe pro ala ser ala ser
 961/321 991/331
 cgc cag gtc gac gga cgt ggt cgc gct atg acg gga atc tgg agc ctt gtc ggg ccg ctc
 arg gln val asp gly arg gly arg ala met thr gly ile trp ser leu val gly pro leu
 ala arg ser thr asp val val ala leu) OPA (arg glu ser gly ala leu ser gly arg ser
 pro gly arg arg thr trp ser arg tyr asp gly asn leu glu pro cys arg ala ala gln
 1021/341 ~~SEQ ID No. 307~~ 1051/351
 aac ata tcg aag atg cac tac ttg agt cgt tgc cag atc ctg tca gat tcc cga ttt ccg
 asn ile ser lys met his tyr leu ser arg cys gln ile leu ser asp ser arg phe pro
 thr tyr arg arg cys thr thr) OPA (val val ala arg ser cys gln ile pro asp phe arg
 his ile glu asp ala leu leu glu ser leu pro asp pro val arg phe pro ile ser ala
 1081/361 ~~SEQ ID No. 308~~ 1111/371
 caa agg agc ggt acg ccc atg acc gtg acc gtt tac act aa)
 gln arg ser gly thr pro met thr val thr val tyr thr)
 lys gly ala val arg pro) OPA pro OPA (pro phe thr leu
 lys glu arg tyr ala his asp arg asp arg leu his) OCH
~~SEQ ID No. 309~~

SEQ ID Nos. 290-316

FIGURE 14G (continued)

1/1 31/11
~~SEQ ID No. 317~~ CAA GCC CGG CCG CGA CTG TTT GCC GTT TTG GGG CTC CTA CCA GAA CAC CAC CTG GCG GCC
~~SEQ ID No. 318~~ gln ala arg pro arg leu phe ala val leu gly leu leu pro glu his his leu ala ala
 61/21 91/31
 GCG CAC CAT GGT GTG CAC CAG TTG CGA TCG GTT CCT CCC GCG CGC GGG CGG CGA CGA CGT
 ala his his gly val his gln leu arg ser val pro pro ala arg gly arg arg arg arg
 121/41 151/51
 CGA TGC CCG CGC CCC GGC GGC GCA GCT GCG TAG CTC GAC CCG GTC GAC GAC GAC GGG GTC
 arg cys pro arg pro gly gly ala ala ala) AMB (leu asp pro val asp asp asp gly val
 181/61 211/71 ~~SEQ ID No. 319~~
 GGC GGA CCA GTC GGC GAT GTC GAG GCG ATG GCA ATA CAG CGC CTT GGT GCG CGG CCA CAC
 gly gly pro val gly asp val glu ala met ala ile gln arg leu gly ala arg pro his
 241/81 271/91
 GTC TGA GGT GGC GAA GAC CAG TCC CGC GCC CAC CGG CAG CCG GAT CCG GAT ACG CGG TAC
 val) OPA (gly gly glu asp gln ser arg ala his arg gln pro asp pro asp thr arg tyr)
~~SEQ ID No. 320~~

SEQ ID Nos 317-320

FIGURE 15A

SEQ ID No. 321 AAG CCC GGC CGC GAC TGT TTG CCG TTT TGG GGC TCC TAC CAG AAC ACC ACC TGG CGG CCG
 lys pro gly arg asp cys leu pro phe trp gly ser tyr gln asn thr thr trp arg pro
 SEQ ID No. 322 62/21 92/31
 CGC ACC ATG GTG TGC ACC AGT TGC GAT CGG TTC CTC CCG CGC GCG GGC GGC GAC GAC GTC
 arg thr met val cys thr ser cys asp arg phe leu pro arg ala gly gly asp asp val
 122/41 152/51
 GAT GCC CGC GCC CCG GCG GCG CAG CTG CGT AGC TCG ACC CGG TCG ACG ACG ACG GGG TCG
 asp ala arg ala pro ala ala gln leu arg ser ser thr arg ser thr thr thr gly ser
 182/61 212/71
 GCG GAC CAG TCG GCG ATG TCG AGG CGA TGG CAA TAC AGC GCC TTG GTG CGC GGC CAC ACG
 ala asp gln ser ala met ser arg arg trp gln tyr ser ala leu val arg gly his thr
 242/81 272/91
 TCT GAG GTG GCG AAG ACC AGT CCC GCG CCC ACC GGC AGC CGG ATC CGG ATA CGC GGT AC
 ser glu val ala lys thr ser pro ala pro thr gly ser arg ile arg ile arg gly)

SEQ ID Nos. 321-322

FIGURE 15B

SEQ ID No. 323 AGC CCG GCC GCG ACT GTT TGC CGT TTT GGG GCT CCT ACC AGA ACA CCA CCT GGC GGC CGC
 ser pro ala ala thr val cys arg phe gly ala pro thr arg thr pro pro gly gly arg
 SEQ ID No. 324 63/21 93/31
 GCA CCA TGG TGT GCA CCA GTT GCG ATC GGT TCC TCC CGC GCG CGG GCG GCG ACG ACG TCG
 ala pro trp cys ala pro val ala ile gly ser ser arg ala arg ala ala thr thr ser
 123/41 153/51
 ATG CCC GCG CCC CGG CGG CGC AGC TGC GTA GCT CGA CCC GGT CGA CGA CGA CGG GGT CGG
 met pro ala pro arg arg arg ser cys val ala arg pro gly arg arg arg arg gly arg
 183/61 213/71
 CGG ACC AGT CGG CGA TGT CGA GGC GAT GGC AAT ACA GCG CCT TGG TGC GCG GCC ACA CGT
 arg thr ser arg arg cys arg gly asp gly asn thr ala pro trp cys ala ala thr arg
 243/81 273/91
 CTG AGG TGG CGA AGA CCA GTC CCG CGC CCA CCG GCA GCC GGA TCC GGA TAC GCG GTA C
 leu arg trp arg arg pro val pro arg pro pro ala ala gly ser gly tyr ala val)

SEQ ID Nos. 323-324

FIGURE 15C

part of the nucleotide sequence of seq15A

SEQ ID NO 325	1/1		31/11
	GGC GGC CGC GCG CCA TGG TGT GCA CCA GTT	GCG ATC GGT TCT CCC GCG CGC GGG CGG CGA	
SEQ ID NO 326	gly gly arg ala pro trp cys ala pro val	ala ile gly ser pro ala arg gly arg arg	
	61/21	91/31	
	CGA CGT CGA TGG CCG CGC CCC GGC GGC TGC	AGC TGC GTA GCT CGA CCC GGT CGA CGA CGA	
	arg arg arg trp pro arg pro gly gly cys	ser cys val ala arg pro gly arg arg arg	
	121/41	151/51	
	CGG GGT CGG CGG GCC AGT CGG CGA TGT CGA	GGC GAT GGC AAT ACA GCG CCT TGG TGC GCG	
	arg gly arg arg ala ser arg arg cys arg	gly asp gly asn thr ala pro trp cys ala	
	181/61	211/71	
	GCC ACA CGT CTG AGG TGG CGA AGA CCA GTC	CCG CGC CCA CCG GCA GCC GGA TC	
	ala thr arg leu arg trp arg arg pro val	pro arg pro pro ala ala gly	

SEQ ID NOS 325-326

FIGURE 15A'

SEQ ID NO 327	1/1		31/11
	GCG GCC GCG CGC CAT GGT GTG CAC CAG TTG	CGA TCG GTT CTC CCG CGC GCG GGC GGC GAC	
SEQ ID NO 328	(ala ala ala arg his gly val his gln leu	arg ser val leu pro arg ala gly gly asp	
	61/21	91/31	
	GAC GTC GAT GGC CGC GCC CCG GCG GCT GCA	GCT GCG TAG CTC GAC CCG GTC GAC GAC GAC	
	asp val asp gly arg ala pro ala ala ala	ala ala)AMB (leu asp pro val asp asp asp	
	121/41	151/51	SEQ ID NO 329
	GGG GTC GGC GGG CCA GTC GGC GAT GTC GAG	GCG ATG GCA ATA CAG CGC CTT GGT GCG CGG	
	gly val gly gly pro val gly asp val glu	ala met ala ile gln arg leu gly ala arg	
	181/61	211/71	
	CCA CAC GTC TGA GGT GGC GAA GAC CAG TCC	CGC GCC CAC CGG CAG CCG GAT C	
	pro his val)OPA (gly gly glu asp gln ser	arg ala his arg gln pro asp)	

SEQ ID NO. 330

SEQ ID NOS. 327-330

FIGURE 15B'

SEQ ID NO. 331	1/1		31/11
	TGG CGG CCG CGC GCC ATG GTG TGC ACC AGT	TGC GAT CGG TTC TCC CGC GCG CGG GCG GCG	
SEQ ID NO. 332	trp arg pro arg ala met val cys thr ser	cys asp arg phe ser arg ala arg ala ala	
	61/21	91/31	
	ACG ACG TCG ATG GCC GCG CCC CGG CGG CTG	CAG CTG CGT AGC TCG ACC CGG TCG ACG ACG	
	thr thr ser met ala ala pro arg arg leu	gln leu arg ser ser thr arg ser thr thr	
	121/41	151/51	
	ACG GGG TCG GCG GGC CAG TCG GCG ATG TCG	AGG CGA TGG CAA TAC AGC GCC TTG GTG CGC	
	thr gly ser ala gly gln ser ala met ser	arg arg trp gln tyr ser ala leu val arg	
	181/61	211/71	
	GGC CAC ACG TCT GAG GTG GCG AAG ACC AGT	CCC GCG CCC ACC GGC AGC CGG ATC	
	gly his thr ser glu val ala lys thr ser	pro ala pro thr gly ser arg ile	

SEQ ID NOS. 331-332

FIGURE 15C'

ORF containing Seq15A' according to Cole et al. (Nature 393:537-544)

1/1
 taa ggt ccg cca acg ctt tac gct cga cgg ccg cca cga gtt ggc cgg cca ctt tca ggc
 61/21
 cgt agt cgc cgc agg gca ggg ctt ccc gcg tcg tct tcg cgg gtt tgt cgg caa agg tgt
 121/41
 arg ser arg arg arg ala gly leu pro ala ser ser ser arg val cys arg gln arg cys
 181/61
 agg ggt agc gtt cgt ggg cgt cga cga cga tgt gca gct cgg gga tgc cgg cgg cgc ggg
 241/81
 arg gly ser val arg gly arg arg arg arg cys ala ala arg gly cys arg arg arg gly
 301/101
 cga cga cga cgt cga tgg ccg cgc ccc ggc ggc tgc agc tgc gta gct cga ccc ggt cga
 361/121
 arg arg arg gly arg arg ala ser arg arg cys arg gly asp gly asn thr ala pro trp
 421/141
 tgc gcg gcc aca cgt ctg agg tgg cga aga cca gtc ccg cgc cca ccg gca gcc gga tca
 481/161
 cys ala ala thr arg leu arg trp arg arg pro val pro arg pro pro ala ala gly ser
 541/181
 ggt agg gca ggc gcg agt ctt cag cgg ggt tgg cgg cga cga gca gct cca cag agt gtg
 601/201
 gly arg ala gly ala ser leu gln arg gly trp arg arg arg ala ala pro gln ser val
 cga agg ggc agg tga
 arg arg gly arg)OPA

SEQ ID Nos. 333-334

FIGURE 150

53/185

R:Rv2530c predicted according to Cole et al. (Nature 393:537-544) and which may be in phase with SEQ15A

SEQ ID No. 335
1/1
gtg acg gca ctg ctc gat gtc aat gtg ctg atc gcg ctg ggc tgg ccg aat cac gtt cac
val thr ala leu leu asp val asn val leu ile ala leu gly trp pro asn his val his
61/21
cat gcg gcc gcg cag cga tgg ttc acg cag ttc tcc tgc aat ggg tgg gcc acc acg ccg
his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr thr pro
121/41
atc acc gag gca ggg tat gtc cga att tca agc aat cgc agt gtg atg cag gtg tgc acc
ile thr glu ala gly tyr val arg ile ser ser asn arg ser val met gln val ser thr
181/61
acg ccg gct atc gcg atc gct cag ttg gcg gcg atg act tct ctt gcc ggg cac acg ttt
thr pro ala ile ala ile ala gln leu ala ala met thr ser leu ala gly his thr phe
241/81
tgg cct gac gat gtg cca ctg atc gtt ggg agc gcc gcc gat cgc gat gcg gtg tcc aac
trp pro asp asp val pro leu ile val gly ser ala gly asp arg asp ala val ser asn
301/101
cac cgt cgg gtc acc gac tgc cat ctc atc gcc ttg gcc gcg cgc tac ggg gcc cgg ttg
his arg arg val thr asp cys his leu ile ala leu ala ala arg tyr gly gly arg leu
361/121
gtc aca ttc gat gcc gca ctg gcc gat tca gca tcc gca gcc ctc gtc gag gtg ttg tag
val thr phe asp ala ala leu ala asp ser ala ser ala gly leu val glu val leu)AMB

SEQ ID Nos. 335-336

FIGURE 15.E

Seq15P: ORF according to Cole et al. (Nature 393:537-544) containing Rv2530c

SEQ ID No. 337
1/1
tga tgt tcc gcc gga tgc gcc gac ggt gac ttc cga gga tgt cgt ccg cgc gct cga gga
OPA/cys ser ala gly cys ala asp gly asp phe arg gly cys arg pro arg ala arg gly
61/21
cga cgt gtg acg gca ctg ctc gat gtc aat gtg ctg atc gcg ctg ggc tgg ccg aat cac
arg arg val thr ala leu leu asp val asn val leu ile ala leu gly trp pro asn his
121/41
gtt cac cat gcg gcc gcg cag cga tgg ttc acg cag ttc tcc tgc aat ggg tgg gcc acc
val his his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr
181/61
acg ccg atc acc gag gca ggg tat gtc cga att tca agc aat cgc agt gtg atg cag gtg
thr pro ile thr glu ala gly tyr val arg ile ser ser asn arg ser val met gln val
241/81
tcg acc acg ccg gct atc gcg atc gct cag ttg gcg gcg atg act tct ctt gcc ggg cac
ser thr thr pro ala ile ala ile ala gln leu ala ala met thr ser leu ala gly his
301/101
acg ttt tgg cct gac gat gtg cca ctg atc gtt ggg agc gcc gcc gat cgc gat gcg gtg
thr phe trp pro asp asp val pro leu ile val gly ser ala gly asp arg asp ala val
361/121
tcc aac cac cgt cgg gtc acc gac tgc cat ctc atc gcc ttg gcc gcg cgc tac ggg gcc
ser asn his arg arg val thr asp cys his leu ile ala leu ala ala arg tyr gly gly
421/141
cgg ttg gtc aca ttc gat gcc gca ctg gcc gat tca gca tcc gca gcc ctc gtc gag gtg
arg leu val thr phe asp ala ala leu ala asp ser ala ser ala gly leu val glu val
481/161
ttg tag
leu)AMB

SEQ ID Nos. 337-338

FIGURE 15.F

Fragment containing Seq15P' and Seq 15F'

1/15 SEQ ID NO. 346 SEQ ID NO. 347 31/11

ID NO. 339-tga tgt tcc gcc gga tgc gcc gac ggt gac ttc cga gga tgt cgt ccg cgc gct cga gga
 OPA (cys ser ala gly cys ala asp gly asp phe arg gly cys arg pro arg ala arg gly
 ID NO. 340 asp val pro pro asp ala pro thr val thr ser glu asp val val arg ala leu glu asp
 ID NO. 348 Met phe arg arg met arg arg arg) OPA (leu pro arg met ser ser ala arg ser arg thr
 61/21 SEQ ID NO. 349 91/31
 cga cgt gtg acg gca ctg ctc gat gtc aat gtg ctg atc gcg ctg ggc tgg ccg aat cac
 arg arg val thr ala leu leu asp val asn val leu ile ala leu gly trp pro asn his
 asp val OPA arg his cys ser met ser met cys OPA ser arg trp ala gly arg ile thr
 thr cys asp gly thr ala arg cys gln cys ala asp arg ala gly leu ala glu ser arg
 121/41 151/51
 gtt cac cat gcg gcc gcg cag cga tgg ttc acg cag ttc tcc tcg aat ggg tgg gcc acc
 val his his ala ala ala gln arg trp phe thr gln phe ser ser asn gly trp ala thr
 phe thr met arg pro arg ser asp gly ser arg ser ser pro arg met gly gly pro pro
 ser pro cys gly arg ala ala met val his ala val leu leu glu trp val gly his his
 181/61 211/71
 acg ccg atc acc gag gca ggg tat gtc cga att tca agc aat cgc agt gtg atg cag gtg
 thr pro ile thr glu ala gly tyr val arg ile ser ser asn arg ser val met gln val
 arg arg ser pro arg gln gly met ser glu phe gln ala ile ala val OPA cys arg cys
 ala asp his arg gly arg val cys pro asn phe lys gln ser gln cys asp ala gly val
 241/81 271/91
 tcg acc acg ccg gct atc gcg atc gct cag ttg gcg gcg atg act tct ctt gcc ggg cac
 ser thr thr pro ala ile ala ile ala gln leu ala ala met thr ser leu ala gly his
 arg pro arg arg leu ser arg ser leu ser trp arg arg OPA leu leu pro gly thr
 asp his ala gly tyr arg asp arg ser val gly gly asp phe ser cys arg ala his
 301/101 331/111
 acg ttt tgg cct gac gat gtg cca ctg atc gtt ggg agc gcc gcc gat cgc gat gcg gtg
 thr phe trp pro asp asp val pro leu ile val gly ser ala gly asp arg asp ala val
 arg phe gly leu thr met cys his OPA ser leu gly ala pro ala ile ala met arg cys
 val leu ala) OPA (arg cys ala thr asp arg trp glu arg arg arg ser arg cys gly val
 361/121 SEQ ID NO. 350 391/131
 tcc aac cac cgt ccg gtc acc gac tgc cat ctc atc gcc ttg gcc gcg cgc tac ggg gcc
 ser asn his arg arg val thr asp cys his leu ile ala leu ala ala arg tyr gly gly
 pro thr thr val gly ser pro thr ala ile ser ser pro trp pro arg ala thr gly ala
 gln pro pro ser gly his arg leu pro ser his arg leu gly arg ala leu arg gly pro
 421/141 451/151
 ccg ttg gtc aca ttc gat gcc gca ctg gcc gat tca gca tcc gca gcc ctc gtc gag gtg
 arg leu val thr phe asp ala ala leu ala asp ser ala ser ala gly leu val glu val
 gly trp ser his ser met pro his trp pro ile gln his pro gln ala ser ser arg cys
 val gly his ile arg cys arg thr gly arg phe ser ile arg arg pro arg arg gly val
 481/161 SEQ ID NO. 341 511/171
 ttg tag tca ccg ggg atg gcc gcc tcg cca gcc ctg cag gat ctg ccg gcg cag gcg ccc
 leu) AMB (ser pro gly met gly gly ser pro gly leu gln asp leu arg ala gln ala pro
 cys ser his arg gly trp ala ala arg gln ala cys arg ile cys gly arg arg arg pro
 val val thr gly asp gly arg leu ala arg pro ala gly ser ala gly ala gly ala pro
 541/181 571/191
 ccg gtc gga cac ccg cag gcc gac gct ttt gcc cca cgc gcg cag ctc gcc gct gct ggg
 pro val gly his arg gln ala asp ala phe gly pro arg ala gln leu gly ala ala gly
 arg ser asp thr gly arg pro thr leu leu ala his ala arg ser ser ala leu leu gly
 gly arg thr pro ala gly arg arg phe trp pro thr arg ala ala arg arg cys trp ala
 601/201 631/211
 ctc ggg ctc gcc gcc agc ccg ctc gaa aac cgt ggt gcc gtc gcc atc gtc gac gaa cca
 leu gly leu gly gly ser arg leu glu asn arg gly gly val gly ile val asp glu pro
 ser gly ser ala ala ala gly ser lys thr val val ala ser ala ser ser thr asn gln
 arg ala arg arg gln pro ala arg lys pro trp trp arg arg his arg arg arg thr arg)

SEQ ID Nos. 339-352

FIGURE 15G

661/221 SEQ ID NO. 342 691/231
 ggt gag ggc ggc ggc tag(ata gcg gta ggt gta ttc ctg ggc gag ctt gcg ggt ttg gca
 gly glu gly gly gly)AMB(ile ala val gly val phe leu gly glu leu ala gly leu ala
 val arg ala ala ala arg AMB arg AMB val tyr ser trp ala ser leu arg val trp gln
 gly arg arg leu asp ser gly arg cys ile pro gly arg ala cys gly phe gly arg
 721/241 751/251
 gaa cac gat cgg cac gtt ggg aaa gcc gat ctg caa ttc ggc cag ccc atc ggc gat cgc
 glu his asp arg his val gly lys ala asp leu gln phe gly gln pro ile gly asp arg
 asn thr ile gly thr leu gly lys pro ile cys asn ser ala ser pro ser ala ile ala
 thr arg ser ala arg trp glu ser arg ser ala ile arg pro ala his arg arg ser pro
 781/261 811/271
 cgt cgg gcg ggc gaa gga gtg cgc gaa gat ctg gta gca gcg gtc ctc gac cac cac ggc
 arg arg ala gly glu gly val arg glu asp leu arg val ala val leu asp his his gly
 val gly arg ala lys glu cys ala lys ile ser glu AMB arg ser ser thr thr thr ala
 ser gly gly arg arg ser ala arg arg ser pro ser ser gly pro arg pro pro arg arg
 841/281 871/291
 ggc ccg tgg cag cgc ggc cag ttc ggt cag ttg gta ttt cag gtt gcc gtt cag cac gcc
 gly pro trp gln arg gly gln phe gly gln leu val phe gln val ala val gln his ala
 ala arg gly ser ala ala ser ser val ser trp tyr phe arg leu pro phe ser thr pro
 pro val ala ala arg pro val arg ser val gly ile ser gly cys arg ser ala arg gln
 901/301 931/311
 aga agt aag gtc cgc caa cgc ttt acg ctg gac ggc cgc cac gag ttg gcc ggc cac ttt
 arg ser lys val arg gln arg phe thr leu asp gly arg his glu leu ala gly his phe
 glu val arg ser ala asn ala leu arg ser thr ala ala thr ser trp pro ala thr phe
 lys)OCH(gly pro pro thr leu tyr ala arg arg pro pro arg val gly arg pro leu ser
 961/321 991/331
 cag gcc gta gtc gcc gca ggg cag ggc ttc ccg cgt cgt ctt cgc ggg ttt gtc ggc aaa
 gln ala val val ala ala gly gln gly phe pro arg arg leu arg gly phe val gly lys
 arg pro AMB ser pro gln gly arg ala ser arg val val phe ala gly leu ser ala lys
 gly arg ser arg arg arg ala gly leu pro ala ser ser ser arg val cys arg gln arg
 1021/341 1051/351
 ggt gta ggg gta gcg ttc gtg ggc gtc gac gat gtg cag ctc ggg gat gcc ggc ggc
 gly val gly val ala phe val gly val asp asp val gln leu gly asp ala gly gly
 val AMB gly AMB arg ser trp ala ser thr thr met cys ser ser gly met pro ala ala
 cys arg gly ser val arg gly arg arg arg arg cys ala ala arg gly cys arg arg arg
 1081/361 1111/371
 gcg ggc ggt ggg ggt gcg cac gcc ccg ccg cga ctg ttt gcg cgt ttt ggg gct ctg cca
 ala gly gly gly gly ala his ala arg pro arg leu phe ala arg phe gly ala leu pro
 arg ala val gly val arg thr pro gly arg asp cys leu arg val leu gly leu cys gln
 gly arg trp gly cys ala arg pro ala ala thr val cys ala phe trp gly ser ala arg
 1141/381 1171/391
 gaa cac cac ctg gcg gcc gcg cgc cat ggt gtg cac cag ttg cga tcg gtt ctc ccg cgc
 glu his his leu ala ala ala arg his gly val his gln leu arg ser val leu pro arg
 asn thr thr trp arg pro arg ala met val cys thr ser cys asp arg phe ser arg ala
 thr pro pro gly gly arg ala pro trp cys ala pro val ala ile gly ser pro ala arg
 1201/401 1231/411
 gcg ggc ggc gac gac gtc gat ggc cgc gcc ccg ccg gct gca gct gcg tag(ctc gac ccg
 ala gly gly asp asp val asp gly arg ala pro ala ala ala ala)AMB(leu asp pro
 arg ala ala thr thr ser met ala ala pro arg arg leu gln leu arg ser ser thr arg
 gly arg arg arg arg arg trp pro arg pro gly gly cys ser cys val ala arg pro gly
 1261/421 1291/431
 gtc gac gac gac ggg gtc ggc ggg cca gtc ggc gat gtc gag gcg atg gca ata cag cgc
 val asp asp asp gly val gly gly pro val gly asp val glu ala met ala ile gln arg
 ser thr thr thr gly ser ala gly gln ser ala met ser arg arg trp gln tyr ser ala
 arg arg arg arg gly arg arg ala ser arg arg cys arg gly asp gly asn thr ala pro

SEQ ID NOS. 334-352

FIGURE 15G (continued 1)

1321/441 SEQ ID No. 344 1351/451
 ctt ggt gcg cgg cca cac gtc tga ggt ggc gaa gac cag tcc cgc gcc cac cgg cag ccg
 leu gly ala arg pro his val) OPA (gly gly glu asp gln ser arg ala his arg gln pro
 leu val arg gly his thr ser glu val ala lys thr ser pro ala pro thr gly ser arg
 trp cys ala ala thr arg leu arg trp arg arg pro val pro arg pro pro ala ala gly
 1381/461 1411/471
 gat cag gta ggg cag gcg cga gtc ttc agc ggg gtt ggc ggc gac gag cag ctc cac aga
 asp gln val gly gln ala arg val phe ser gly val gly gly asp glu gln leu his arg
 ile arg AMB gly arg arg glu ser ser ala gly leu ala ala thr ser ser ser thr glu
 ser gly arg ala gly ala ser leu gln arg gly trp arg arg arg ala ala pro gln ser
 1441/481 SEQ ID No. 1471/491
 gtg tga ggg tac ggg cgg cgt acg gca acg gtg aag cag gca ctc cga cga acc cat cgt
 val) OPA (gly tyr gly arg arg thr ala thr val lys gln ala leu arg arg thr his arg
 cys glu gly thr gly gly val arg gln arg OPA ser arg his ser asp glu pro ile val
 val arg val arg ala ala tyr gly asn gly glu ala gly thr pro thr asn pro ser ser
 1501/501
 cac gtc gaa ggg gca ggt ga)
 his val glu gly ala gly)
 thr ser lys gly gln val
 arg arg arg gly arg) OPA

SEQ ID Nos. 334-352 (continued 2)

FIGURE 15G (continued (2))

31/11
 20 ID No. 353 TGC GCA TGC CGA CCA GTG TGG TTG GCC GGA GTT CGT TTG TTC GCG ATT GCC TCA ACG ATT
 20 ID No. 354 (cys ala cys arg pro val trp leu ala gly val arg leu phe ala ile ala ser thr ile
 61/21 91/31
 CGA TAT AAC CAC TCT AGT CAC ATC AAC CAC ACT CGT ACC ATC GAG CGT GTG GGT TCA TGC
 arg tyr asn his ser ser his ile asn his thr arg thr ile glu arg val gly ser cys
 121/41 151/51
 CAT GCA TTC GCG ACC GCG GGA GCC GGC GAA CCC GGC GCC ACA CAT AAT CCA GAT TGA GGA
 his ala phe ala thr ala gly ala gly glu pro gly ala thr his asn pro asp) OPA (gly
 181/61 211/71 SEQ ID No. 355
 GAC TTC CGT GCC GAA CCG ACG CCG ACG CAA GCT TTC GAC AGC CAT GAG CGC GGT CGC CGC
 asp phe arg ala glu pro thr pro thr gln ala phe asp ser his glu arg gly arg arg
 241/81 271/91
 CCT GGC AGT TGC AAG TCC TTG TGC ATA TTT TCT TGT TCT CTA CGA ATC AAC CGA AAC GAC CGA
 pro gly ser cys lys ser leu cys ile phe ser cys leu arg ile asn arg asn asp arg
 301/101 331/111
 GCG GCC CGA GCA CCA TGA ATT CAA GCA GGC GGC GGT GTT GAC CGA CCT GCC CGG CGA GCT
 ala ala arg ala pro) OPA (ile gln ala gly gly gly val asp arg pro ala arg arg ala
 361/121 SEQ ID No. 356 391/131
 GAT GTC CGC GCT ATC GCA GGG GTT GTC CCA GTT CGG GAT C
 asp val arg ala ile ala gly val val pro val arg asp)

SEQ ID Nos. 353-356

FIGURE 16A

30 ID No. 357	GCG CAT GCC GAC CAG TGT GGT TGG CCG GAG	32/11	TTC GTT TGT TCG CGA TTG CCT CAA CGA TTC
30 ID No. 358	(ala his ala asp gln cys gly trp pro glu	62/21	phe val cys ser arg leu pro gln arg phe
	GAT ATA ACC ACT CTA GTC ACA TCA ACC ACA	92/31	CTC GTA CCA TCG AGC GTG TGG GTT CAT GCC
	asp ile thr thr leu val thr ser thr thr	122/41	leu val pro ser ser val trp val his ala
	ATG CAT TCG CGA CCG CGG GAG CCG GCG AAC	152/51	CCG GCG CCA CAC ATA ATC CAG ATT GAG GAG
	met his ser arg pro arg glu pro ala asn	182/61	pro ala pro his ile ile gln ile glu glu
	ACT TCC GTG CCG AAC CGA CGC CGA CGC AAG	212/71	CTT TCG ACA GCC ATG AGC GCG GTC GCC GCC
	thr ser val pro asn arg arg arg arg lys	242/81	leu ser thr ala met ser ala val ala ala
	CTG GCA GTT GGA AGT CCT TGT GCA TAT TTT	272/91	CTT GTC TAC GAA TCA ACC GAA ACG ACC GAG
	leu ala val ala ser pro cys ala tyr phe	302/101	leu val tyr glu ser thr glu thr thr glu
	CGG CCC GAG CAC CAT GAA TTC AAG CAG GCG	332/111	GCG GTG TTG ACC GAC CTG CCC GGC GAG CTG
	arg pro glu his his glu phe lys gln ala	362/121	ala val leu thr asp leu pro gly glu leu
	ATG TCC GCG CTA TCG CAG GGG TTG TCC CAG	392/131	TCC GGG ATC
	met ser ala leu ser gln gly leu ser gln		phe gly ile)

SEQ ID Nos. 357-358

FIGURE 16B

33/11
 359 ID No. 359 CGC ATG CCG ACC AGT GTG GTT GGC CGG AGT TCG TTT GTT CGC GAT TGC CTC AAC GAT TCG
 360 ID No. 360 arg met pro thr ser val val gly arg ser ser phe val arg asp cys leu asn asp ser
 63/21 93/31
 ATA TAA CCA CTC TAG TCA CAT CAA CCA CAC TCG TAC CAT CGA GCG TGT GGG TTC ATG CCA
 ile) OCH pro leu AMB (ser his gln pro his ser tyr his arg ala cys gly phe met pro
 123/41 153/51
 TGC ATT CGC GAC CGC GGC AGC CGG CGA ACC CGG CGC CAC ACA TAA TCC AGA TTG AGG AGA
 cys ile arg asp arg gly ser arg arg thr arg arg his thr) OCH (ser arg leu arg arg
 183/61 213/71
 CTT CCG TGC CGA ACC GAC GCC GAC GCA AGC TTT CGA CAG CCA TGA GCG CGG TCG CCG CCC
 leu pro cys arg thr asp ala asp ala ser phe arg gln pro) OPA (ala arg ser pro pro
 243/81 273/91
 TGG CAG TTG CAA GTC CTT GTG CAT ATT TTC TTG TCT ACG AAT CAA CCG AAA CGA CCG AGC
 trp gln leu gln val leu val his ile phe leu ser thr asn gln pro lys arg pro ser
 303/101 333/111
 GGC CCG AGC ACC ATG AAT TCA AGC AGG CGG CGG TGT TGA CCG ACC TGC CCG GCG AGC TGA
 gly pro ser thr met asn ser ser arg arg arg cys) OPA (pro thr cys pro ala ser) OPA
 363/121 393/131
 TGT CCG CGC TAT CGC AGG GGT TGT CCC AGT TCG GGA TC
 (cys pro arg tyr arg arg gly cys pro ser ser gly)
 350 ID No. 926
 350 ID No. 927
 350 ID No. 928
 350 ID No. 929
 350 ID No. 930

SEQ ID Nos. 359-360, 926-930

FIGURE 16C

31/11
 SEQ ID No. 361 GCG GGC CAC CGA TCA GTC GAT CGG GTG GTT TCC GCT CCA TCA GCC CGG AAT TGA GGT GCC
 SEQ ID No. 362 ala gly his arg ser val asp arg val val ser ala pro ser ala arg asn) OPA (gly ala
 61/21 91/31
 GCA GTG ACG ACA CCA GCG CAG GAC GCG CCG TTG GTG TTT CCC TCT GTT GCT TTC CCG TCC
 ala val thr thr pro ala gln asp ala pro leu val phe pro ser val ala phe pro ser
 121/41 151/51
 GGC TCG CCT TTT TTT CAT CAA CGT TGG ACT GCC GCA GTG GCG ATG TTG GTC GCC GGC GTG
 gly ser pro phe phe his gln arg trp thr ala ala val ala met leu val ala gly val
 181/61 211/71
 TTC GGT CAC CTG ACG GTC GGG ATG TTC CTT GGG TCT CGG GTT GCT GCT GGG TTT GCT CAA
 phe gly his leu thr val gly met phe leu gly ser arg val ala ala gly phe ala gln
 241/81 271/91
 TGC CCT GCT GGT GCG GCG TTC GGC CGA GTC GAT CAC CGC CAA AGA GCA CCC GTT AAA ACG
 cys pro ala gly ala ala phe gly arg val asp his arg gln arg ala pro val lys thr
 301/101 331/111
 GTC GAT GGC CCT CAA CTC GGC ATC GCG ACT GGC GAT TAT CAC CAT GCC TCG GGC TGA TC
 val asp gly pro gln leu gly ile ala thr gly asp tyr his his ala ser gly) OPA

SEQ ID Nos. 361-363

FIGURE 17A

32/11
 SEQ ID No. 364 CCG GCC ACC GAT CAG TCG ATC GGG TGG TTT CCG CTC CAT CAG CCC GGA ATT GAG GTG CCG
 SEQ ID No. 365 (arg ala thr asp gln ser ile gly trp phe pro leu his gln pro gly ile glu val pro
 62/21 92/31
 CAG TGA CGA CAC CAG CGC AGG ACG CGC CGT TGG TGT TTC CCT CTG TTG CTT TCC CGT CCG
 gln) OPA (arg his gln arg arg thr arg arg trp cys phe pro leu leu leu ser arg pro
 122/41 152/51
 GCT CGC CTT TTT TTC ATC AAC GTT GGA CTG CCG CAG TGG CGA TGT TGG TCG CCG GCG TGT
 ala arg leu phe phe ile asn val gly leu pro gln trp arg cys trp ser pro ala cys
 182/61 212/71
 TCG GTC ACC TGA CGG TCG GGA TGT TCC TTG GGT CTC GGG TTG CTG CTG GGT TTG CTC AAT
 ser val thr) OPA (arg ser gly cys ser leu gly leu gly leu leu leu gly leu leu asn
 242/81 272/91
 GCC CTG CTG GTG CGG CGT TCG GCC GAG TCG ATC ACC GCC AAA GAG CAC CCG TTA AAA CCG
 ala leu leu val arg arg ser ala glu ser ile thr ala lys glu his pro leu lys arg
 302/101 332/111
 TCG ATG GCC CTC AAC TCG GCA TCG CGA CTG GCG ATT ATC ACC ATG CCT CGG GCT GAT C
 ser met ala leu asn ser ala ser arg leu ala ile ile thr met pro arg ala asp)

SEQ ID Nos. 364-367

FIGURE 17B

ID No. 368 33/11
 GGG CCA CCG ATC AGT CGA TCG GGT GGT TTC CGC TCC ATC AGC CCG GAA TTG AGG TGC CGC
 (gly pro pro ile ser arg ser gly gly phe arg ser ile ser pro glu leu arg cys arg
 ID No. 369 63/21 93/31
 AGT GAC GAC ACC AGC GCA GGA CGC GCC GTT GGT GTT TCC CTC TGT TGC TTT CCC GTC CGG
 ser asp asp thr ser ala gly arg ala val gly val ser leu cys cys phe pro val arg
 123/41 153/51
 CTC GCC TTT TTT TCA TCA ACG TTG GAC TGC CGC AGT GGC GAT GTT GGT CGC CGG CGT GTT
 leu ala phe phe ser ser thr leu asp cys arg ser gly asp val gly arg arg arg val
 183/61 213/71
 CGG TCA CCT GAC GGT CGG GAT GTT CCT TGG GTC TCG GGT TGC TGC TGG GTT TGC TCA ATG
 arg ser pro asp gly arg asp val pro trp val ser gly cys cys trp val cys ser met
 243/81 273/91
 CCC TGC TGG TGC GGC GTT CGG CCG AGT CGA TCA CCG CCA AAG AGC ACC CGT TAA AAC GGT
 pro cys trp cys gly val arg pro ser arg ser pro pro lys ser thr arg) OCH (asn gly
 303/101 333/111 SEQ ID No. 370
 CGA TGG CCC TCA ACT CGG CAT CGC GAC TGG CGA TTA TCA CCA TGC CTC GGG CTG ATC
 arg trp pro ser thr arg his arg asp trp arg leu ser pro cys leu gly leu ile)

SEQ ID Nos. 368-370

FIGURE 17C

part of the nucleotide sequence of seq17A

ID No. 371 1/1 31/11
 ggc tag aac ccc gaa gga gac ctc gcg ggt tgc cgg ccc ccg gcc cat cgg atg cgt atc
 gly AMB (asn pro glu gly asp leu ala gly cys arg pro pro ala his arg met arg ile
 61/21 SEQ ID No. 372 91/31
 cgg tcg cgc cga ttc acg acc gac ata ggg agc tac ccc ttg ggt gat tcc ggt gcg acg
 arg ser arg arg phe thr thr asp ile gly ser tyr pro leu gly asp ser gly ala thr
 121/41 151/51
 act gcg ata cgc tcg gcg ggc cac cga tca gtc gat cgg gtg gtt tcc gct cca tca gcc
 thr ala ile arg ser ala gly his arg ser val asp arg val val ser ala pro ser ala
 181/61 211/71
 cgg aat tga ggt gcc gca gtg acg aca cca gcg cag gac gcg ccg ttg gtg ttt ccc tct
 arg asn) OPA (gly ala ala val thr thr pro ala gln asp ala pro leu val phe pro ser
 241/81 SEQ ID No. 373 271/91
 gtt gct ttc cgt ccg gtt cgc ctt ttt ttc atc aac gtt gga ctg gcc gca gtg gcg atg
 val ala phe arg pro val arg leu phe phe ile asn val gly leu ala ala val ala met
 301/101 331/111
 ttg gtc gcc ggc gtg ttc ggt cac ctg acg gtc ggg atg ttc ttg ggt ctc ggg ttg ctg
 leu val ala gly val phe gly his leu thr val gly met phe leu gly leu gly leu leu
 361/121 391/131
 ctg ggt ttg ctc aat gcc ctg ctg gtg cgg cgt tcg gcc gag tcg atc acc gcc aaa gag
 leu gly leu leu asn ala leu leu val arg arg ser ala glu ser ile thr ala lys glu
 421/141 451/151
 cac ccg tta aaa cgg tcg atg gcc ctc aac tcg gca tcg cga ctg gcg att atc acc atc
 his pro leu lys arg ser met ala leu asn ser ala ser arg leu ala ile ile thr ile
 481/161
 ctc ggg ctg atc
 leu gly leu ile)

SEQ ID Nos. 371-373

FIGURE 17A'

1/1
 SEQ ID NO. 374 gct aga acc ccg aag gag acc tcg cgg gtt gcc gcc ccc ccg ccc atc gga tgc gta tcc
 (ala arg thr pro lys glu thr ser arg val ala gly pro arg pro ile gly cys val ser
 61/21
 SEQ ID NO. 375 ggt cgc gcc gat tca cga ccg aca tag gga gct acc cct tgg gtg att ccg gtg cga cga
 gly arg ala asp ser arg pro thr) AMB (gly ala thr pro trp val ile pro val arg arg
 121/41
 ctg cga tac gct cgg cgg gcc acc gat cag tcg atc ggg tgg ttt ccg ctc cat cag ccc
 leu arg tyr ala arg arg ala thr asp gln ser ile gly trp phe pro leu his gln pro
 181/61
 gga att gag gtg ccg cag tga cga cac cag cgc agg acg cgc cgt tgg tgt ttc cct ctg
 gly ile glu val pro gln) OPA (arg his gln arg arg thr arg arg trp cys phe pro leu
 241/81
 ttg ctt tcc gtc cgg ttc gcc ttt ttt tca tca acg ttg gac tgg ccg cag tgg cga tgt
 leu leu ser val arg phe ala phe phe ser ser thr leu asp trp pro gln trp arg cys
 301/101
 tgg tcg ccg gcg tgt tcg gtc acc tga cgg tcg gga tgt tct tgg gtc tcg ggt tgc tgc
 trp ser pro ala cys ser val thr) OPA (arg ser gly cys ser trp val ser gly cys cys
 361/121
 tgg gtt tgc tca atg ccc tgc tgg tgc gcc gtt cgg ccg agt cga tca ccg cca aag agc
 trp val cys ser met pro cys trp cys gly val arg pro ser arg ser pro pro lys ser
 421/141
 acc cgt taa aac ggt cga tgg ccc tca act cgg cat cgc gac tgg cga tta tca cca tcc
 thr arg) OCH (asn gly arg trp pro ser thr arg his arg asp trp arg leu ser pro ser
 481/161
 tcg gcc tga tc
 ser gly) OPA

SEQ ID Nos. 374-379

FIGURE 17B'

1/1
 SEQ ID NO. 380 cta gaa ccc cga agg aga cct cgc ggg ttg ccg gcc ccc gcc cca tcg gat gcg tat ccg
 (leu glu pro arg arg arg pro arg gly leu pro ala pro gly pro ser asp ala tyr pro
 61/21
 SEQ ID NO. 381 gtc gcg ccg att cac gac cga cat agg gag cta ccc ctt ggg tga ttc ccg tgc gac gac
 val ala pro ile his asp arg his arg glu leu pro leu gly) OPA (phe arg cys asp asp
 121/41
 tgc gat acg ctc gcc ggg cca ccg atc agt cga tcg ggt ggt ttc cgc tcc atc agc ccg
 cys asp thr leu gly gly pro pro ile ser arg ser gly gly phe arg ser ile ser pro
 181/61
 gaa ttg agg tgc cgc agt gac gac acc agc gca gga cgc gcc gtt ggt gtt tcc ctc tgt
 glu leu arg cys arg ser asp asp thr ser ala gly arg ala val gly val ser leu cys
 241/81
 tgc ttt ccg tcc ggt tcg cct ttt ttt cat caa cgt tgg act gcc cgc agt gcc gat gtt
 cys phe pro ser gly ser pro phe phe his gln arg trp thr gly arg ser gly asp val
 301/101
 ggt cgc cgg cgt gtt cgg tca cct gac ggt cgg gat gtt ctt ggg tct cgg gtt gct gct
 gly arg arg arg val arg ser pro asp gly arg asp val leu gly ser arg val ala ala
 361/121
 ggg ttt gct caa tgc cct gct ggt gcg gcg ttc gcc cga gtc gat cac cgc caa aga gca
 gly phe ala gln cys pro ala gly ala ala phe gly arg val asp his arg gln arg ala
 421/141
 ccc gtt aaa acg gtc gat gcc cct caa ctc gcc atc gcg act gcc gat tat cac cat cct
 pro val lys thr val asp gly pro gln leu gly ile ala thr gly asp tyr his his pro
 481/161
 cgg gct gat c
 arg ala asp)

SEQ ID Nos. 380-382

FIGURE 17C'

61/185

sequence Rv1303 predicted by Cole et al. (Nature 393:537-544) and partially containing Seq17A'

1/1
 31/11
 atg acg aca cca gcg cag gac gcg ccg ttg gtg ttt ccc tct gtt gct ttc cgt ccg gtt
 met thr thr pro ala gln asp ala pro leu val phe pro ser val ala phe arg pro val
 61/21 91/31
 cgc ctt ttt ttc atc aac gtt gga ctg gcc gca gtg gcg atg ttg gtc gcc ggc gtg ttc
 arg leu phe phe ile asn val gly leu ala ala val ala met leu val ala gly val phe
 121/41 151/51
 ggt cac ctg acg gtc ggg atg ttc ttg ggt ctc ggg ttg ctg ctg ggt ttg ctc aat gcc
 gly his leu thr val gly met phe leu gly leu gly leu leu leu gly leu leu asn ala
 181/61 211/71
 ctg ctg gtg ccg cgt tcg gcc gag tcg atc acc gcc aaa gag cac ccg tta aaa ccg tcg
 leu leu val arg arg ser ala glu ser ile thr ala lys glu his pro leu lys arg ser
 241/81 271/91
 atg gcc ctc aac tcg gca tcg cga ctg gcg att atc acc atc ctc ggg ctg atc atc gcc
 met ala leu asn ser ala ser arg leu ala ile ile thr ile leu gly leu ile ile ala
 301/101 331/111
 tac att ttc ccg ccc gct gga ttg ggc gtc gtg ttc ggg ctg gca ttc ttc cag gtg ctg
 tyr ile phe arg pro ala gly leu gly val val phe gly leu ala phe phe gln val leu
 361/121 391/131
 ctg gtg gca acg acg gcc ctg ccg gtc ctg aag aag ctg cgc act gcg acc gag gaa ccg
 leu val ala thr thr ala leu pro val leu lys lys leu arg thr ala thr glu glu pro
 421/141 451/151
 gtc gca act tat tct tcc aat ggc cag acc ggg gga tcg gaa gga agg agc gcc agc gat
 val ala thr tyr ser ser asn gly gln thr gly gly ser glu gly arg ser ala ser asp
 481/161
 gac tga
 asp)OPA

SEQ ID Nos. 383-384

FIGURE 17D

Orf according to Cole et al. (Nature 393:537-544) and containing Rv1303

1/1
 31/11
 tga ggt gcc gca gtg acg aca cca gcg cag gac gcg ccg ttg gtg ttt ccc tct gtt gct
 OPA gly ala ala val thr thr pro ala gln asp ala pro leu val phe pro ser val ala
 61/21 91/31
 ttc cgt ccg gtt cgc ctt ttt ttc atc aac gtt gga ctg gcc gca gtg gcg atg ttg gtc
 phe arg pro val arg leu phe phe ile asn val gly leu ala ala val ala met leu val
 121/41 151/51
 gcc ggc gtg ttc ggt cac ctg acg gtc ggg atg ttc ttg ggt ctc ggg ttg ctg ctg ggt
 ala gly val phe gly his leu thr val gly met phe leu gly leu gly leu leu leu gly
 181/61 211/71
 ttg ctc aat gcc ctg ctg gtg ccg cgt tcg gcc gag tcg atc acc gcc aaa gag cac ccg
 leu leu asn ala leu leu val arg arg ser ala glu ser ile thr ala lys glu his pro
 241/81 271/91
 tta aaa ccg tcg atg gcc ctc aac tcg gca tcg cga ctg gcg att atc acc atc ctc ggg
 leu lys arg ser met ala leu asn ser ala ser arg leu ala ile ile thr ile leu gly
 301/101 331/111
 ctg atc atc gcc tac att ttc ccg ccc gct gga ttg ggc gtc gtg ttc ggg ctg gca ttc
 leu ile ile ala tyr ile phe arg pro ala gly leu gly val val phe gly leu ala phe
 361/121 391/131
 ttc cag gtg ctg ctg gtg gca acg acg gcc ctg ccg gtc ctg aag aag ctg cgc act gcg
 phe gln val leu leu val ala thr thr ala leu pro val leu lys lys leu arg thr ala
 421/141 451/151
 acc gag gaa ccg gtc gca act tat tct tcc aat ggc cag acc ggg gga tcg gaa gga agg
 thr glu glu pro val ala thr tyr ser ser asn gly gln thr gly gly ser glu gly arg
 481/161
 agc gcc agc gat gac tga
 ser ala ser asp asp)OPA

SEQ ID Nos. 385-386

FIGURE 17E

62/185

20 ID No. 387 GTC GAA CAG GTA CGG AAG GCG CCG TCG GTC 31/11
 20 ID No. 388 (val glu gln val arg lys ala pro ser val ala arg ser ala gly ile ser cys ser ala
 61/21 91/31
 AGC CAG CGG CCG TTA ACG TGG CCG AAC AGG TCG TCT TGG GGT CGG GCA TCA GCG TCG ATG
 ser gln arg pro leu thr trp pro asn arg ser ser trp gly arg ala ser ala ser met
 121/41 151/51
 TGG CTC AGG TCG ATA CCC GAG GGG ATG GCA AGT GTC ACC CCG CCA TCC TTC CAC CTC TTT
 trp leu arg ser ile pro glu gly met ala ser val thr pro pro ser phe his leu phe
 181/61 211/71
 TCG GGT GCA ACG ATC GGG CCA TGC CTG ACG GGG AGC AGA GCC AGC CAC CGG CCC AAG AAG
 ser gly ala thr ile gly pro cys leu thr gly ser arg ala ser his arg pro lys lys
 241/81 271/91
 ATG CGG AAG ACG ACT CGC GGC CCG ACG CCG CGG AGG CCG CCG CGG CCG AAC CCA AAT CAT
 met arg lys thr thr arg gly pro thr pro arg arg pro pro arg pro asn pro asn his
 301/101 331/111
 CAG CCG GTC CCG ATG TTC TCG ACC TAC GGT ATC GCC TCG ACA CTA CTC GGC GTG CTA TCG
 gln pro val pro met phe ser thr tyr gly ile ala ser thr leu leu gly val leu ser
 361/121
 GTC GCC GCG GTC GTG CTG GGT GCG ATG ATC
 val ala ala val val leu gly ala met ile)

SEQ ID Nos. 387-388

FIGURE 18A

20 ID No. 389 TCG AAC AGG TAC GGA AGG CGC CGT CGG TCG 32/11
 20 ID No. 390 (ser asn arg tyr gly arg arg arg arg ser leu gly pro leu val ser arg val gln pro
 62/21 92/31
 GCC AGC GGC CGT TAA CGT GGC CGA ACA GGT CGT CTT GGG GTC GGG CAT CAG CGT CGA TGT
 ala ser gly arg) OCH (arg gly arg thr gly arg leu gly val gly his gln arg arg cys
 122/41 152/51
 GGC TCA GGT CGA TAC CCG AGG GGA TGG CAA GTG TCA CCC CGC CAT CCT TCC ACC TCT TTT
 gly ser gly arg tyr pro arg gly trp gln val ser pro arg his pro ser thr ser phe
 182/61 212/71
 CGG GTG CAA CGA TCG GGC CAT GCC TGA CGG GGA GCA GAG CCA GCC ACC GGC CCA AGA AGA
 arg val gln arg ser gly his ala) OPA (arg gly ala glu pro ala thr gly pro arg arg
 242/81 272/91
 TGC GGA AGA CGA CTC GCG GCC CGA CGC CGC GGA GGC CGC CGC GGC CGA ACC CAA ATC ATC
 cys gly arg arg leu ala ala arg arg arg gly gly arg arg gly arg thr gln ile ile
 302/101 332/111
 AGC CGG TCC CGA TGT TCT CGA CCT ACG GTA TCG CCT CGA CAC TAC TCG GCG TGC TAT CGG
 ser arg ser arg cys ser arg pro thr val ser pro arg his tyr ser ala cys tyr arg
 362/121
 TCG CCG CGG TCG TGC TGG GTG CGA TGA TC
 ser pro arg ser cys trp val arg) OPA

SEQ ID Nos. 389-392

FIGURE 18B

63/185

30 ID No. 393 3/1
 CGA ACA GGT ACG GAA GGC GCC GTC GGT CGC TCG GTC CGC TGG TAT CTC GTG TTC AGC CAG
 20 ID No. 394 (arg thr gly thr glu gly ala val gly arg ser val arg trp tyr leu val phe ser gln
 63/21
 CCA GCG GCC GTT AAC GTG GCC GAA CAG GTC GTC TTG GGG TCG GGC ATC AGC GTC GAT GTG
 pro ala ala val asn val ala glu gln val val leu gly ser gly ile ser val asp val
 123/41
 GCT CAG GTC GAT ACC CGA GGG GAT GGC AAG TGT CAC CCC GCC ATC CTT CCA CCT CTT TTC
 ala gln val asp thr arg gly asp gly lys cys his pro ala ile leu pro pro leu phe
 183/61
 GGG TGC AAC GAT CGG GCC ATG CCT GAC GGG GAG CAG AGC CAG CCA CCG GCC CAA GAA GAT
 gly cys asn asp arg ala met pro asp gly glu gln ser gln pro pro ala gln glu asp
 243/81
 GCG GAA GAC GAC TCG CGG CCC GAC GCC GCG GAG GCC GCC GCG GCC GAA CCC AAA TCA TCA
 ala glu asp asp ser arg pro asp ala ala glu ala ala ala glu pro lys ser ser
 303/101
 GCC GGT CCC GAT GTT CTC GAC CTA CGG TAT CGC CTC GAC ACT ACT CGG CGT GCT ATC GGT
 ala gly pro asp val leu asp leu arg tyr arg leu asp thr thr arg arg ala ile gly
 363/121
 CGC CGC GGT CGT GCT GGG TGC GAT GAT C
 arg arg gly arg ala gly cys asp asp)

SEQ ID Nos. 393-394

FIGURE 18C

part of the nucleotide sequence of seq18A

1/1
 30 ID No. 395 GAA GGC GCC GTC GGT CGC TCG GTC CGC TGG TAT CTC GTG TTC AGC CAG CCA GCG GCC GTT
 20 ID No. 396 (glu gly ala val gly arg ser val arg trp tyr leu val phe ser gln pro ala ala val
 61/21
 AAC GTG GCC GAA CAG GTC GTC TTG GGG TCG GGC ATC AGC GTC GAT GTG GCT CAG GTC GAT
 asn val ala glu gln val val leu gly ser gly ile ser val asp val ala gln val asp
 121/41
 ACC CGA GGG GAT GGC AAG TGT CAC CCC GCC ATC CTT CCA CCT CTT TTC GGG TGC AAC GAT
 thr arg gly asp gly lys cys his pro ala ile leu pro pro leu phe gly cys asn asp
 181/61
 CGG GCC ATG CCT GAC GGG GAG CAG AGC CAG CCA CCG GCC CAA GAA GAT GCG GAA GAC GAC
 arg ala met pro asp gly glu gln ser gln pro pro ala gln glu asp ala glu asp asp
 241/81
 TCG CGG CCC GAC GCC GCG GAG GCC GCC GCG GCC GAA CCC AAA TCA TCA GCC GGT CCG ATG
 ser arg pro asp ala ala glu ala ala ala ala glu pro lys ser ser ala gly pro met
 301/101
 TTC TCG ACC TAC GGT ATC GCC TCG ACA CTA CTC GGC GTG CTA TCG GTC GCC GCG GTC GTG
 phe ser thr tyr gly ile ala ser thr leu leu gly val leu ser val ala ala val val
 361/121
 CTG GGT GCG ATG ATC
 leu gly ala met ile)

SEQ ID Nos. 395-396

FIGURE 18A'

1/1	31/11
SEQ ID No. 397	CGG AAG GCG CCG TCG GTC GCT CGG TCC GCT GGT ATC TCG TGT TCA GCC AGC CAG CGG CCG
SEQ ID No. 398	(arg lys ala pro ser val ala arg ser ala gly ile ser cys ser ala ser gln arg pro
61/21	91/31
TTA ACG TGG CCG AAC AGG TCG TCT TGG GGT CGG GCA TCA GCG TCG ATG TGG CTC AGG TCG	
leu thr trp pro asn arg ser ser trp gly arg ala ser ala ser met trp leu arg ser	
121/41	151/51
ATA CCC GAG GGG ATG GCA AGT GTC ACC CCG CCA TCC TTC CAC CTC TTT TCG GGT GCA ACG	
ile pro glu gly met ala ser val thr pro pro ser phe his leu phe ser gly ala thr	
181/61	211/71
ATC GGG CCA TGC CTG ACG GGG AGC AGA GCC AGC CAC CGG CCC AAG AAG ATG CGG AAG ACG	
ile gly pro cys leu thr gly ser arg ala ser his arg pro lys lys met arg lys thr	
241/81	271/91
ACT CGC GGC CCG ACG CCG CGG AGG CCG CCG CGG CCG AAC CCA AAT CAT CAG CCG GTC CGA	
thr arg gly pro thr pro arg arg pro pro arg pro asn pro asn his gln pro val arg	
301/101	331/111
TGT TCT CGA CCT ACG GTA TCG CCT CGA CAC TAC TCG GCG TGC TAT CGG TCG CCG CGG TCG	
cys ser arg pro thr val ser pro arg his tyr ser ala cys tyr arg ser pro arg ser	
361/121	
TGC TGG GTG CGA TGA TC	
cys trp val arg)OPA	

SEQ ID Nos. 397-398

FIGURE 18B'

1/1	31/11
SEQ ID No. 399	GGA AGG CGC CGT CGG TCG CTC GGT CCG CTG GTA TCT CGT GTT CAG CCA GCC AGC GGC CGT
SEQ ID No. 400	(gly arg arg arg arg ser leu gly pro leu val ser arg val gln pro ala ser gly arg)
61/21	91/31
TAA CGT GGC CGA ACA GGT CGT CTT GGG GTC GGG CAT CAG CGT CGA TGT GGC TCA GGT CGA	
SEQ ID No. 401	OCH (arg gly arg thr gly arg leu gly val gly his gln arg arg cys gly ser gly arg
121/41	151/51
TAC CCG AGG GGA TGG CAA GTG TCA CCC CGC CAT CCT TCC ACC TCT TTT CGG GTG CAA CGA	
tyr pro arg gly trp gln val ser pro arg his pro ser thr ser phe arg val gln arg	
181/61	211/71
TCG GGC CAT GCC TGA CGG GGA GCA GAG CCA GCC ACC GGC CCA AGA AGA TGC GGA AGA CGA	
ser gly his ala)OPA (arg gly ala glu pro ala thr gly pro arg arg cys gly arg arg	
241/81	271/91
CTC GCG GCC CGA CGC CGC GGA GGC CGC CGC GGC CGA ACC CAA ATC ATC AGC CGG TCC GAT	
leu ala ala arg arg arg gly gly arg arg gly arg thr gln ile ile ser arg ser asp	
301/101	331/111
GTT CTC GAC CTA CGG TAT CGC CTC GAC ACT ACT CGG CGT GCT ATC GGT CGC CGC GGT CGT	
val leu asp leu arg tyr arg leu asp thr thr arg arg ala ile gly arg arg gly arg	
361/121	
GCT GGG TGC GAT GAT C	
ala gly cys asp asp)	

SEQ ID Nos. 399-402

FIGURE 18C'

sequence Rv0199 predicted by Cole et al. (Nature 393:537-544) and containing seq18A'

1/1	31/11
SEQ ID No. 403 atg cct gac ggg gag cag agc cag cca ccg gcc caa gaa gat gcg gaa gac gac tcg cgg	
EQ ID No. 404 (Met pro asp gly glu gln ser gln pro pro ala gln glu asp ala glu asp asp ser arg	
61/21	91/31
ccc gac gcc gcg gag gcc gcc gcg gcc gaa ccc aaa tca tca gcc ggt ccg atg ttc tcg	
pro asp ala ala glu ala ala ala ala glu pro lys ser ser ala gly pro met phe ser	
121/41	151/51
acc tac ggt atc gcc tcg aca cta ctc ggc gtg cta tcg gtc gcc gcg gtc gtg ctg ggt	
thr tyr gly ile ala ser thr leu leu gly val leu ser val ala ala val val leu gly	
181/61	211/71
gcg atg atc tgg tcc gca cac cgc gat gac tcc ggc gag cgt acc tac ctg acc cgg gtc	
ala met ile trp ser ala his arg asp asp ser gly glu arg thr tyr leu thr arg val	
241/81	271/91
atg ctg acc gcc gct gaa tgg acg gcc gtg ctg atc aac atg aac gcc gac aac atc gat	
met leu thr ala ala glu trp thr ala val leu ile asn met asn ala asp asn ile asp	
301/101	331/111
gcc agc ctg cag cga ctg cac gac gga acg gtc ggt caa ctc aac acc gac ttc gac gct	
ala ser leu gln arg leu his asp gly thr val gly gln leu asn thr asp phe asp ala	
361/121	391/131
gtc gtg cag ccc tac cgg cag gtg gtg gag aag ttg cgg acg cac agc agc ggc agg atc	
val val gln pro tyr arg gln val val glu lys leu arg thr his ser ser gly arg ile	
421/141	451/151
gag gcg gta gcg atc gat acg gtg cac cgc gag ctg gat acc cag tcc ggt gcc gcc cga	
glu ala val ala ile asp thr val his arg glu leu asp thr gln ser gly ala ala arg	
481/161	511/171
ccg gta gta acc acg aaa ttg cca ccg ttt gcc act cgc acc gac tcg gtg ctg ctg gtc	
pro val val thr thr lys leu pro pro phe ala thr arg thr asp ser val leu leu val	
541/181	571/191
gcg acg tcg gtc agt gag aac gcc ggc gcc aaa ccc cag acc gtg cac tgg aac ttg cgg	
ala thr ser val ser glu asn ala gly ala lys pro gln thr val his trp asn leu arg	
601/201	631/211
ctc gat gtc tcc gat gtg gac ggc aag ctg atg atc tcc cgg ttg gag tcg att cga tga	
leu asp val ser asp val asp gly lys leu met ile ser arg leu glu ser ile arg)OPA	

SEQ ID Nos. 403-404

FIGURE 18D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv0199

1/1

31/11

⑤ ID No. 405 taa tcc gat gcc gga ttg ggt gaa atg cac caa gta acg ggt cga gtc ttt gga atc ggt
 OCH (ser asp ala gly leu gly glu met his gln val thr gly arg val phe gly ile gly
 ⑤ ID No. 406 61/21 91/31
 atc gac ata gac tcc gat gcc gcc gcc cac gcc gcc acg ttg cag agt gcc aag ggc gcc
 ile asp ile asp ser asp ala ala ala his ala gly thr leu gln ser ala lys gly gly
 121/41 151/51
 gcc caa ttc ggt gcc gtc gcc cgc gct gtc aat cgt gcc caa ttc gtc gtg cag cgg ttg
 gly gln phe gly gly val gly arg ala val asn arg gly gln phe val val gln arg leu
 181/61 211/71
 cac ccc tgc gcg ctc gac gcc ttc ctc gtc gag gaa gct gcc gta gag gtc gcc gat gcg
 his pro cys ala leu asp gly phe leu val glu glu ala gly val glu val ala asp ala
 241/81 271/91
 ctg cgc atc ggt gcc tac cgc agc acc tgc ttg gct gcc ctg gat gat cag gtc tcg cac
 leu arg ile gly ala tyr arg ser thr cys leu ala gly leu asp asp gln val ser his
 301/101 331/111
 ttg tgt ctc gcc gcg gtc gaa cag gct acg gaa gcc gcc gtc ggt cgc tcg gtc cgc tgg
 leu cys leu gly ala val glu gln ala thr glu gly ala val gly arg ser val arg trp
 361/121 391/131
 tat ctc gtg ttc agc cag cca gcg gcc gtt aac gtg gcc gaa cag gtc gtc ttg ggg tcg
 tyr leu val phe ser gln pro ala ala val asn val ala glu gln val val leu gly ser
 421/141 451/151
 gcc atc agc gtc gat gtg gct cag gtc gat acc cga ggg gat gcc aag tgt cac ccc gcc
 gly ile ser val asp val ala gln val asp thr arg gly asp gly lys cys his pro ala
 481/161 511/171
 atc ctt cca cct ctt ttc ggg tgc aac gat ccg gcc atg cct gac ggg gag cag agc cag
 ile leu pro pro leu phe gly cys asn asp arg ala met pro asp gly glu gln ser gln
 541/181 571/191
 cca ccg gcc caa gaa gat gcg gaa gac gac tcg ccg ccc gac gcc gcg gag gcc gcc gcg
 pro pro ala gln glu asp ala glu asp asp ser arg pro asp ala ala glu ala ala ala
 601/201 631/211
 gcc gaa ccc aaa tca tca gcc ggt ccg atg ttc tcg acc tac ggt atc gcc tcg aca cta
 ala glu pro lys ser ser ala gly pro met phe ser thr tyr gly ile ala ser thr leu
 661/221 691/231
 ctc gcc gtg cta tcg gtc gcc gcg gtc gtg ctg ggt gcg atg atc tgg tcc gca cac cgc
 leu gly val leu ser val ala ala val val leu gly ala met ile trp ser ala his arg
 721/241 751/251
 gat gac tcc gcc gag cgt acc tac ctg acc ccg gtc atg ctg acc gcc gct gaa tgg acg
 asp asp ser gly glu arg thr tyr leu thr arg val met leu thr ala ala glu trp thr
 781/261 811/271
 gcc gtg ctg atc aac atg aac gcc gac aac atc gat gcc agc ctg cag cga ctg cac gac
 ala val leu ile asn met asn ala asp asn ile asp ala ser leu gln arg leu his asp
 841/281 871/291
 gga acg gtc ggt caa ctc aac acc gac ttc gac gct gtc gtg cag ccc tac ccg cag gtg
 gly thr val gly gln leu asn thr asp phe asp ala val val gln pro tyr arg gln val
 901/301 931/311
 gtg gag aag ttg ccg acg cac agc agc gcc agg atc gag gcg gta gcg atc gat acg gtg
 val glu lys leu arg thr his ser ser gly arg ile glu ala val ala ile asp thr val
 961/321 991/331
 cac cgc gag ctg gat acc cag tcc ggt gcc gcc cga ccg gta gta acc acg aaa ttg cca
 his arg glu leu asp thr gln ser gly ala ala arg pro val val thr thr lys leu pro
 1021/341 1051/351
 ccg ttt gcc act cgc acc gac tcg gtg ctg ctg gtc gcg acg tcg gtc agt gag aac gcc
 pro phe ala thr arg thr asp ser val leu leu val ala thr ser val ser glu asn ala
 1081/361 1111/371
 gcc gcc aaa ccc cag acc gtg cac tgg aac ttg ccg ctc gat gtc tcc gat gtg gac gcc
 gly ala lys pro gln thr val his trp asn leu arg leu asp val ser asp val asp gly
 1141/381 1171/391
 aag ctg atg atc tcc ccg ttg gag tcg att cga tga
 lys leu met ile ser arg leu glu ser ile arg) OPA

SEQ ID Nos. 405-406

FIGURE 18E

SEQ ID No. 407 GTT GCG CAA CGG GGT GAG CAC CGA CGC GAT GAT GGC GCA ACT ATC GAA ACT GCA GGA CAT
 (val ala gln arg gly glu his arg arg asp asp gly ala thr ile glu thr ala gly his
 61/21 91/31
 CGC CAA CGC CAA CGA CGG CAC TCG CGC GGT GGG CAC CCC TGG CTA TCA GGC CAG CGT CGA
 arg gln arg gln arg arg his ser arg gly gly his pro trp leu ser gly gln arg arg
 121/41 151/51
 CTA TGT GGT AAA CAC ACT GCG CAA CAG CGG TTT TGA TGT GCA AAC CCC GGA GTT CTC CGC
 leu cys gly lys his thr ala gln gln arg phe)OPA(cys ala asn pro gly val leu arg
 181/61 211/71 SEQ ID No. 408
 TCG CGT GTT CAA GGC CGA AAA AGG GGT GGT GAC CCT CGG CGG CAA CAC CGT GGA GGC GAG
 ser arg val gln gly arg lys arg gly gly asp pro arg arg gln his arg gly gly glu
 241/81 271/91
 GGC GCT CGA GTA CAG CCT CGG CAC ACC GCC GGA CGG GGT GAC GGG CCC GCT GGT GGC TGC
 gly ala arg val gln pro arg his thr ala gly arg gly asp gly pro ala gly gly cys
 301/101 331/111
 CCC CGC CGA CGA CAG TCC GGG CTG CAG TCC GTC GGA CTA CGA CAG GCT GCC GGT GTC CGG
 pro arg arg arg gln ser gly leu gln ser val gly leu arg gln ala ala gly val arg
 361/121
 TGC GGT GGT GCT GGT AGA TC
 cys gly gly ala gly arg)

SEQ ID Nos 407-409

FIGURE 19A

SEQ ID No. 410 TTG GCG AAC GGG GTG AGC ACC GAC GCG ATG ATG GCG CAA CTA TCG AAA CTG CAG GAC ATC
 (leu arg asn gly val ser thr asp ala met met ala gln leu ser lys leu gln asp ile
 62/21 92/31
 GCC AAC GCC AAC GAC GGC ACT CGC GCG GTG GGC ACC CCT GGC TAT CAG GCC AGC GTC GAC
 ala asn ala asn asp gly thr arg ala val gly thr pro gly tyr gln ala ser val asp
 122/41 152/51
 TAT GTG GTA AAC ACA CTG CGC AAC AGC GGT TTT GAT GTG CAA ACC CCG GAG TTC TCC GCT
 tyr val val asn thr leu arg asn ser gly phe asp val gln thr pro glu phe ser ala
 182/61 212/71
 CGC GTG TTC AAG GCC GAA AAA GGG GTG GTG ACC CTC GGC GGC AAC ACC GTG GAG GCG AGG
 arg val phe lys ala glu lys gly val val thr leu gly gly asn thr val glu ala arg
 242/81 272/91
 GCG CTC GAG TAC AGC CTC GGC ACA CCG CCG GAC GGG GTG ACG GGC CCG CTG GTG GCT GCC
 ala leu glu tyr ser leu gly thr pro pro asp gly val thr gly pro leu val ala ala
 302/101 332/111
 CCC GCC GAC GAC AGT CCG GGC TGC AGT CCG TCG GAC TAC GAC AGG CTG CCG GTG TCC GGT
 pro ala asp asp ser pro gly cys ser pro ser asp tyr asp arg leu pro val ser gly
 362/121
 GCG GTG GTG CTG GTA GAT C
 ala val val leu val asp)

SEQ ID Nos 410-411

FIGURE 19B

33/11
 SEQ ID NO. 412 TGC GCA ACG GGG TGA GCA CCG ACG CGA TGA TGG CGC AAC TAT CGA AAC TGC AGG ACA TCG
 SEQ ID NO. 413 (cys ala thr gly) OPA (ala pro thr arg) OPA (trp arg asn tyr arg asn cys arg thr ser
 63/21 SEQ ID NO. 414 SEQ ID NO. 415 93/31
 CCA ACG CCA ACG ACG GCA CTC GCG CGG TGG GCA CCC CTG GCT ATC AGG CCA GCG TCG ACT
 pro thr pro thr thr ala leu ala arg trp ala pro leu ala ile arg pro ala ser thr
 123/41 153/51
 ATG TGG TAA ACA CAC TGC GCA ACA GCG GTT TTG ATG TGC AAA CCC CGG AGT TCT CCG CTC
 met trp) OCH (thr his cys ala thr ala val leu met cys lys pro arg ser ser pro leu
 183/61 SEQ ID NO. 416 213/71
 GCG TGT TCA AGG CCG AAA AAG GGG TGG TGA CCC TCG GCG GCA ACA CCG TGG AGG CGA GGG
 ala cys ser arg pro lys lys gly trp) OPA (pro ser ala ala thr pro trp arg arg gly
 243/81 SEQ ID NO. 417 73/91
 CGC TCG AGT ACA GCC TCG GCA CAC CGC CGG ACG GGG TGA CGG GCC CGC TGG TGG CTG CCC
 arg ser ser thr ala ser ala his arg arg thr gly) OPA (arg ala arg trp trp leu pro
 303/101 333/111 SEQ ID NO. 418
 CCG CCG ACG ACA GTC CGG GCT GCA GTC CGT CGG ACT ACG ACA GGC TGC CGG TGT CCG GTG
 pro pro thr thr val arg ala ala val arg arg thr thr thr gly cys arg cys pro val
 363/121
 CGG TGG TGC TGG TAG ATC
 arg trp cys trp) AMB ile

SEQ ID NOS. 412-418

FIGURE 19C

part of the nucleotide sequence of seq19A

1/1 31/11
 SEQ ID NO. 419 CTA TCG AAA CTG CAG GAC ATC GCC AAC GCC AAC GAC GGC ACT CGC GCG GTG GGC ACC CCT
 SEQ ID NO. 420 (leu ser lys leu gln asp ile ala asn ala asn asp gly thr arg ala val gly thr pro
 61/21 91/31
 GGC TAT CAG GCC AGC GTC GAC TAT GTG GTA AAC ACA CTG CGC AAC AGC GGT TTT GAT GTG
 gly tyr gln ala ser val asp tyr val val asn thr leu arg asn ser gly phe asp val
 121/41 151/51
 CAA ACC CCG GAG TTC TCC GCT CGC GTG TTC AAG GCC GAA AAA GGG GTG GTG ACC CTC GGC
 gln thr pro glu phe ser ala arg val phe lys ala glu lys gly val val thr leu gly
 181/61 211/71
 GGC AAC ACC GTG GAG GCG AGG GCG CTC GAG TAC AGC CTC GGC ACA CCG CCG GAC GGG GTG
 gly asn thr val glu ala arg ala leu glu tyr ser leu gly thr pro pro asp gly val
 241/81 271/91
 ACG GGC CCG CTG GTG GCT GCC CCC GCC GAC GAC AGT CCG GGC TGC AGT CCG TCG GAC TAC
 thr gly pro leu val ala ala pro ala asp asp ser pro gly cys ser pro ser asp tyr
 301/101 331/111
 GAC AGG CTG CCG GTG TCC GGT GCG GTG GTG CTG GTA GAT C
 asp arg leu pro val ser gly ala val val leu val asp)

SEQ ID NOS. 419-420

FIGURE 19A'

1/1 31/11
 SEQ ID No. 421 TAT CGA AAC TGC AGG ACA TCG CCA ACG CCA ACG ACG GCA CTC GCG CGG TGG GCA CCC CTG
 SEQ ID No. 422 (tyr arg asn cys arg thr ser pro thr pro thr thr ala leu ala arg trp ala pro leu
 61/21 91/31
 GCT ATC AGG CCA GCG TCG ACT ATG TGG TAA ACA CAC TGC GCA ACA GCG GTT TTG ATG TGC
 ala ile arg pro ala ser thr met trp) OCH (thr his cys ala thr ala val leu met cys
 121/41 SEQ ID No. 423 151/51
 AAA CCC CGG AGT TCT CCG CTC GCG TGT TCA AGG CCG AAA AAG GGG TGG TGA CCC TCG GCG
 lys pro arg ser ser pro leu ala cys ser arg pro lys lys gly trp) OPA (pro ser ala
 181/61 211/71 SEQ ID No. 424
 GCA ACA CCG TGG AGG CGA GGG CGC TCG AGT ACA GCC TCG GCA CAC CGC CGG ACG GGG TGA
 ala thr pro trp arg arg gly arg ser ser thr ala ser ala his arg arg thr gly) OPA
 241/81 271/91
 CGG GCC CGC TGG TGG CTG CCC CCG CCG ACG ACA GTC CGG GCT GCA GTC CGT CGG ACT ACG
 SEQ ID No. 425 (arg ala arg trp trp leu pro pro pro thr thr val arg ala ala val arg arg thr thr
 301/101 331/111
 ACA GGC TGC CGG TGT CCG GTG CGG TGG TGC TGG TAG ATC
 thr gly cys arg cys pro val arg trp cys trp) AMB ile

SEQ ID Nos. 421-425

FIGURE 19B'

1/1 31/11
 SEQ ID No. 426 ATC GAA ACT GCA GGA CAT CGC CAA CGC CAA CGA CGG CAC TCG CGC GGT GGG CAC CCC TGG
 SEQ ID No. 427 (ile glu thr ala gly his arg gln arg gln arg arg his ser arg gly gly his pro trp
 61/21 91/31
 CTA TCA GGC CAG CGT CGA CTA TGT GGT AAA CAC ACT GCG CAA CAG CGG TTT TGA TGT GCA
 leu ser gly gln arg arg leu cys gly lys his thr ala gln gln arg phe) OPA (cys ala
 121/41 151/51 SEQ ID No. 428
 AAC CCC GGA GTT CTC CGC TCG CGT GTT CAA GGC CGA AAA AGG GGT GGT GAC CCT CGG CGG
 asn pro gly val leu arg ser arg val gln gly arg lys arg gly gly asp pro arg arg
 181/61 211/71
 CAA CAC CGT GGA GGC GAG GGC GCT CGA GTA CAG CCT CGG CAC ACC GCC GGA CGG GGT GAC
 gln his arg gly gly glu gly ala arg val gln pro arg his thr ala gly arg gly asp
 241/81 271/91
 GGG CCC GCT GGT GGC TGC CCC CGC CGA CGA CAG TCC GGG CTG CAG TCC GTC GGA CTA CGA
 gly pro ala gly gly cys pro arg arg arg gln ser gly leu gln ser val gly leu arg
 301/101 331/111
 CAG GCT GCC GGT GTC CGG TGC GGT GGT GCT GGT AGA TC
 gln ala ala gly val arg cys gly gly ala gly arg)

SEQ ID Nos. 426-428

FIGURE 19C'

31/11

30 ID No. 429
D-ID No. 430

61/21	ctg acg acg ggc tgt atc cgg tgg tct acg	aac aaa tcc agg atg atg ccg gcg
121/41	leu thr thr gly cys ile arg trp ser thr	val leu ala val ala val val val ala phe
181/61	gcc gca gag ttc gcc gtt gcg ttg cgc aac	cag tcg cgg ccc gtt gtt aac ggc ccc gct
241/81	ala ala glu phe ala val ala leu arg asn	arg val ser thr asp ala met met ala his
301/101	cta tcg aaa ctg cag gac atc gcc aac gcc	aac gac ggc act cgc gcg gtg ggc acc cct
361/121	leu ser lys leu gln asp ile ala asn ala	asn asp gly thr arg ala val gly thr pro
421/141	ggc tat cag gcc agc gtc gac tat gtg gta	aac aca ctg cgc aac agc ggt ttt gat gtg
481/161	gly tyr gln ala ser val asp tyr val val	asn thr leu arg asn ser gly phe asp val
541/181	caa acc ccg gag ttc tcc gct cgc gtg ttc	aag gcc gaa aaa ggg gtg gtg acc ctc gcc
601/201	gln thr pro glu phe ser ala arg val phe	lys ala glu lys gly val val thr leu gly
661/221	ggc aac acc gtg gag gcg agg gcg ctc gag	tac agc ctc ggc aca ccg ccg gac ggg gtg
721/241	gly asn thr val glu ala arg ala leu glu	tyr ser leu gly thr pro pro asp gly val
781/261	acg ggc ccg ctg gtg gct gcc ccc gcc gac	gac agt ccg ggc tgc agt ccg tcg gac tac
841/281	thr gly pro leu val ala ala pro ala asp	asp ser pro gly cys ser pro ser asp tyr
901/301	gac agg ctg ccg gtg tcc ggt gcg gtg gtg	ctg gta gat cgc ggc gtc tgt cct ttt gcc
961/321	asp arg leu pro val ser gly ala val val	leu val asp arg gly val cys pro phe ala
	cag aag gaa gac gca gcc gcg cag cgc ggt	gcg gtg gcg ctg atc att gct gac aac atc
	gln lys glu asp ala ala ala gln arg gly	ala val ala leu ile ile ala asp asn ile
	gac gag cag gcg atg ggc ggc acc ctg ggg	gct aat acc gac gtc aag atc ccg gtg gtg
	asp glu gln ala met gly gly thr leu gly	ala asn thr asp val lys ile pro val val
	agt gtc acc aag tcg gtc gga ttc cag cta	cgc gga cag tct ggg cca acc acc gtc aag
	ser val thr lys ser val gly phe gln leu	arg gly gln ser gly pro thr thr val lys
	ctc acg gcg agc acc caa agt ttc aag gcc	cgc aac gtc atc gcg cag acg aag acg ggg
	leu thr ala ser thr gln ser phe lys ala	arg asn val ile ala gln thr lys thr gly
	tcg tcg gcc aac gtg gtg atg gca ggt gcg	cat ttg gac agc gtt ccg gaa gga ccc gcc
	ser ser ala asn val val met ala gly ala	his leu asp ser val pro glu gly pro gly
	atc aac gac aac ggc tcg gga gtg gct gcg	gtt ctg gaa acg gca gtg cag ctg ggg aac
	ile asn asp asn gly ser gly val ala ala	val leu glu thr ala val gln leu gly asn
	tca ccg cat gtg tcc aac gcg gta cgg ttc	gcc ttc tgg ggc gcc gag gaa ttc gcc ctg
	ser pro his val ser asn ala val arg phe	ala phe trp gly ala glu glu phe gly leu
	att ggg tca cga aac tac gtc gag tcg ctg	gac atc gac gcg ctc aaa ggc atc gcg ctg
	ile gly ser arg asn tyr val glu ser leu	asp ile asp ala leu lys gly ile ala leu

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1021/341	1051/351
tat ctg aac ttc gac atg ttg gcg tcg ccg	aac ccg ggt tac ttc acc tac gac ggt gac
tyr leu asn phe asp met leu ala ser pro	asn pro gly tyr phe thr tyr asp gly asp
1081/361	1111/371
cag tcg ctg ccg cta gac gcc cgc ggt cag	ccg gtg gtg ccc gaa ggc tcg gcc ggt atc
gln ser leu pro leu asp ala arg gly gln	pro val val pro glu gly ser ala gly ile
1141/381	1171/391
gag cgc acg ttc gtc gcc tat ctg aag atg	gcc ggc aag acc gcg cag gac acc tcg ttc
glu arg thr phe val ala tyr leu lys met	ala gly lys thr ala gln asp thr ser phe
1201/401	1231/411
gac ggt cgg tcc gac tac gac ggc ttc acg	ctg gcg ggt atc cct tcg ggt ggc ctg ttc
asp gly arg ser asp tyr asp gly phe thr	leu ala gly ile pro ser gly gly leu phe
1261/421	1291/431
tcc ggc gct gag gtc aag aag tcc gcc gag	caa gcc gag ctc tgg ggc ggc acc gcc gac
ser gly ala glu val lys lys ser ala glu	gln ala glu leu trp gly gly thr ala asp
1321/441	1351/451
gag cct ttc gat ccc aac tat cac cag aag	aca gac acc ctg gac cat atc gac cgc acc
glu pro phe asp pro asn tyr his gln lys	thr asp thr leu asp his ile asp arg thr
1381/461	1411/471
gcg ctc ggt atc aac ggc gct ggc gtc gcg	tac gcg gtg ggt ttg tat gcg cag gac ctc
ala leu gly ile asn gly ala gly val ala	tyr ala val gly leu tyr ala gln asp leu
1441/481	1471/491
ggc ggc ccc aac ggg gtt ccg gtc atg gcg	gac cgc acc cgc cac ctg att gcc aaa ccg
gly gly pro asn gly val pro val met ala	asp arg thr arg his leu ile ala lys pro)
1501/501	
tga	
OPA	

SEQ ID Nos. 429-450 (continued)

FIGURE 19D (continued)

ORF according to Cole et al. (Nature 393:537-544) and containing Rv0418

1/1	31/11
30 ID No. 431 tag gcc att caa cgc tct gtt cgt ttg att ggt cgg tgg gat gcg aaa gct gcg cgg cga	
AMB ala ile gln arg ser val arg leu ile gly arg trp asp ala lys ala ala arg arg	
20 ID No. 432 61/21	91/31
cag gcg cgg tct aat ctg ggc gcg atg gtg aac aaa tcc agg atg atg ccg gcg gtg ctg	
gln ala arg ser asn leu gly ala met val asn lys ser arg met met pro ala val leu	
121/41	151/51
gcc gtg gct gtg gtc gtc gca ttc ctg acg acg ggc tgt atc cgg tgg tct acg cag tgg	
ala val ala val val val ala phe leu thr thr gly cys ile arg trp ser thr gln ser	
181/61	211/71
cgg ccc gtt gtt aac ggc ccc gct gcc gca gag ttc gcc gtt gcg ttg cgc aac cgg gtg	
arg pro val val asn gly pro ala ala ala glu phe ala val ala leu arg asn arg val	
241/81	271/91
agc acc gac gcg atg atg gcg cac cta tcg aaa ctg cag gac atc gcc aac gcc aac gac	
ser thr asp ala met met ala his leu ser lys leu gln asp ile ala asn ala asn asp	
301/101	331/111
ggc act cgc gcg gtg ggc acc cct ggc tat cag gcc agc gtc gac tat gtg gta aac aca	
gly thr arg ala val gly thr pro gly tyr gln ala ser val asp tyr val val asn thr	
361/121	391/131
ctg cgc aac agc ggt ttt gat gtg caa acc ccg gag ttc tcc gct cgc gtg ttc aag gcc	
leu arg asn ser gly phe asp val gln thr pro glu phe ser ala arg val phe lys ala	
421/141	451/151
gaa aaa ggg gtg gtg acc ctc ggc ggc aac acc gtg gag gcg agg gcg ctc gag tac agc	
glu lys gly val val thr leu gly gly asn thr val glu ala arg ala leu glu tyr ser	
481/161	511/171
ctc ggc aca ccg ccg gac ggg gtg acg ggc ccg ctg gtg gct gcc ccc gcc gac gac agt	
leu gly thr pro pro asp gly val thr gly pro leu val ala ala pro ala asp asp ser	
541/181	571/191
ccg ggc tgc agt ccg tcg gac tac gac agg ctg ccg gtg tcc ggt gcg gtg gtg ctg gta	
pro gly cys ser pro ser asp tyr asp arg leu pro val ser gly ala val val leu val	
601/201	631/211
gat cgc ggc gtc tgt cct ttt gcc cag aag gaa gac gca gcc gcg cag cgc ggt gcg gtg	
asp arg gly val cys pro phe ala gln lys glu asp ala ala ala gln arg gly ala val	
661/221	691/231
gcg ctg atc att gct gac aac atc gac gag cag gcg atg ggc ggc acc ctg ggg gct aat	
ala leu ile ile ala asp asn ile asp glu gln ala met gly gly thr leu gly ala asn	
721/241	751/251
acc gac gtc aag atc ccg gtg gtg agt gtc acc aag tcg gtc gga ttc cag cta cgc gga	
thr asp val lys ile pro val val ser val thr lys ser val gly phe gln leu arg gly	
781/261	811/271
cag tct ggg cca acc acc gtc aag ctc acg gcg agc acc caa agt ttc aag gcc cgc aac	
gln ser gly pro thr thr val lys leu thr ala ser thr gln ser phe lys ala arg asn	
841/281	871/291
gtc atc gcg cag acg aag acg ggg tcg tcg gcc aac gtg gtg atg gca ggt gcg cat ttg	
val ile ala gln thr lys thr gly ser ser ala asn val val met ala gly ala his leu	
901/301	931/311
gac agc gtt ccg gaa gga ccc ggc atc aac gac aac ggc tcg gga gtg gct gcg gtt ctg	
asp ser val pro glu gly pro gly ile asn asp asn gly ser gly val ala ala val leu	
961/321	991/331
gaa acg gca gtg cag ctg ggg aac tca ccg cat gtg tcc aac gcg gta cgg ttc gcc ttc	
glu thr ala val gln leu gly asn ser pro his val ser asn ala val arg phe ala phe	

SEQ ID Nos. 431-432

FIGURE 19E

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1021/341	1051/351
tgg ggc gcc gag gaa ttc ggc ctg att ggg	tca cga aac tac gtc gag tcg ctg gac atc
trp gly ala glu glu phe gly leu ile gly	ser arg asn tyr val glu ser leu asp ile
1081/361	1111/371
gac gcg ctc aaa ggc atc gcg ctg tat ctg	aac ttc gac atg ttg gcg tcg ccg aac ccg
asp ala leu lys gly ile ala leu tyr leu	asn phe asp met leu ala ser pro asn pro
1141/381	1171/391
ggt tac ttc acc tac gac ggt gac cag tcg	ctg ccg cta gac gcc cgc ggt cag ccg gtg
gly tyr phe thr tyr asp gly asp gln ser	leu pro leu asp ala arg gly gln pro val
1201/401	1231/411
gtg ccc gaa ggc tcg gcc ggt atc gag cgc	acg ttc gtc gcc tat ctg aag atg gcc ggc
val pro glu gly ser ala gly ile glu arg	thr phe val ala tyr leu lys met ala gly
1261/421	1291/431
aag acc gcg cag gac acc tcg ttc gac ggt	cgg tcc gac tac gac ggc ttc acg ctg gcg
lys thr ala gln asp thr ser phe asp gly	arg ser asp tyr asp gly phe thr leu ala
1321/441	1351/451
ggt atc cct tcg ggt ggc ctg ttc tcc ggc	gct gag gtc aag aag tcc gcc gag caa gcc
gly ile pro ser gly gly leu phe ser gly	ala glu val lys lys ser ala glu gln ala
1381/461	1411/471
gag ctc tgg ggc ggc acc gcc gac gag cct	ttc gat ccc aac tat cac cag aag aca gac
glu leu trp gly gly thr ala asp glu pro	phe asp pro asn tyr his gln lys thr asp
1441/481	1471/491
acc ctg gac cat atc gac cgc acc gcg ctc	ggt atc aac ggc gct ggc gtc gcg tac gcg
thr leu asp his ile asp arg thr ala leu	gly ile asn gly ala gly val ala tyr ala
1501/501	1531/511
gtg ggt ttg tat gcg cag gac ctc ggc ggc	ccc aac ggg gtt ccg gtc atg gcg gac cgc
val gly leu tyr ala gln asp leu gly gly	pro asn gly val pro val met ala asp arg
1561/521	
acc cgc cac ctg att gcc aaa ccg tga	
thr arg his leu ile ala lys pro) OPA	

SEQ ID Nos. 431-432 (continued)

FIGURE 19E (continued)

EO ID No. 433	CGA GAC AGT GGT GCG GGA CAC TTG AGT TCG	31/11	GCT GCT AAC GAC GCC AGA GTC GCC CGC TTC
EO ID No. 434	(arg asp ser gly ala gly his leu ser ser	61/21	ala ala asn asp ala arg val ala arg phe
	CGC GGT GTG GGA CTC ACG TTC GGT GAG GGT	91/31	ACA GCG GAC CTT CGA GCA CGC AAT ATC GTG
	arg gly val gly leu thr phe gly glu gly	151/51	thr ala asp leu arg ala arg asn ile val
	121/41		GGC CGG CTG GCA ACC GTC GGT TTC GAC GTT
	gly arg leu ala thr val gly phe asp val	211/71	gly asp asp pro ser phe met asn arg ser)
	181/61		TGA GCT CCC CGT TTT GCT GGA TGC CCA GGC
EO ID No. 435	OPA (ala pro arg phe ala gly cys pro gly	271/91	ACC GCC GGT ACT GCT GCG CTT AAG CTT GTC
	241/81		GCA CAT GGT GCC GGC AGG GAG GAA CAG TGG
	ala his gly ala gly arg glu glu gln trp	331/111	GCA AGC AGC TAG CCG CGC TCG CCG CGC TGG
	301/101	SEQ ID No. 436	ala ser ser) AMB (pro arg ser pro arg trp
	TCG GTG CGT GCA TGC TCG CAG CCG GAT GCA		CCA ACG TGG TCG ACG GGA CCG CCG TGG CTG
	ser val arg ala cys ser gln pro asp ala		pro thr trp ser thr gly pro pro trp leu
	361/121		CCG ACA AAT CCG GAC CAC TGC ATC AGG ATC
	pro thr asn pro asp his cys ile arg ile)		

SEQ ID Nos. 433-436

FIGURE 20A

SEQ ID NO. 437- GAG ACA GTG GTG CGG GAC ACT TGA GTT CGG CTG CTA ACG ACG CCA GAG TCG CCC GCT TCC
 (glu thr val val arg asp thr) OPA (val arg leu leu thr thr pro glu ser pro ala ser
 SEQ ID NO. 438 62/21 SEQ ID NO. 439 92/31
 GCG GTG TGG GAC TCA CGT TCG GTG AGG GTA CAG CGG ACC TTC GAG CAC GCA ATA TCG TGG
 ala val trp asp ser arg ser val arg val gln arg thr phe glu his ala ile ser trp
 122/41 152/51
 GCC GGC TGG CAA CCG TCG GTT TCG ACG TTG GTG ACG ACC CCT CGT TCA TGA ATC GTT CTT
 ala gly trp gln pro ser val ser thr leu val thr thr pro arg ser) OPA (ile val leu
 182/61 212/71 SEQ ID NO. 440
 GAG CTC CCC GTT TTG CTG GAT GCC CAG GCA CCG CCG GTA CTG CTG CGC TTA AGC TTG TCG
 glu leu pro val leu leu asp ala gln ala pro pro val leu leu arg leu ser leu ser
 242/81 272/91
 CAC ATG GTG CCG GCA GGG AGG AAC AGT GGG CAA GCA GCT AGC CGC GCT CGC CGC GCT GGT
 his met val pro ala gly arg asn ser gly gln ala ala ser arg ala arg arg ala gly
 302/101 332/111
 CGG TGC GTG CAT GCT CGC AGC CGG ATG CAC CAA CGT GGT CGA CGG GAC CGC CGT GGC TGC
 arg cys val his ala arg ser arg met his gln arg gly arg arg asp arg arg gly cys
 362/121
 CGA CAA ATC CGG ACC ACT GCA TCA GGA TC
 arg gln ile arg thr thr ala ser gly)

SEQ ID Nos. 437-440

FIGURE 20B

SEQ ID NO. 441- AGA CAG TGG TGC GGG ACA CTT GAG TTC GGC TGC TAA CGA CGC CAG AGT CGC CCG CTT CCG
 (arg gln trp cys gly thr leu glu phe gly cys) OCH (arg arg gln ser arg pro leu pro
 SEQ ID NO. 442 63/21 SEQ ID NO. 443 93/31
 CGG TGT GGG ACT CAC GTT CGG TGA GGG TAC AGC GGA CCT TCG AGC ACG CAA TAT CGT GGG
 arg cys gly thr his val arg) OPA (gly tyr ser gly pro ser ser thr gln tyr arg gly
 123/41 153/51
 CCG GCT GGC AAC CGT CGG TTT CGA CGT TGG TGA CGA CCC CTC GTT CAT GAA TCG TTC TTG
 pro ala gly asn arg arg phe arg arg trp) OPA (arg pro leu val his glu ser phe leu
 183/61 213/71 SEQ ID NO. 445
 AGC TCC CCG TTT TGC TGG ATG CCC AGG CAC CGC CGG TAC TGC TGC GCT TAA GCT TGT CGC
 ser ser pro phe cys trp met pro arg his arg arg tyr cys cys ala) OCH (ala cys arg
 243/81 273/91 SEQ ID NO. 446
 ACA TGG TGC CGG CAG GGA GGA ACA GTG GGC AAG CAG CTA GCC GCG CTC GCC GCG CTG GTC
 thr trp cys arg gln gly gly thr val gly lys gln leu ala ala leu ala ala leu val
 303/101 333/111
 GGT GCG TGC ATG CTC GCA GCC GGA TGC ACC AAC GTG GTC GAC GGG ACC GCC GTG GCT GCC
 gly ala cys met leu ala ala gly cys thr asn val val asp gly thr ala val ala ala
 363/121
 GAC AAA TCC GGA CCA CTG CAT CAG GAT C
 asp lys ser gly pro leu his gln asp)

SEQ ID Nos. 441-446

FIGURE 20C

part of the nucleotide sequence of seq20A

1/1 31/11
 SEQ ID No. 447 TGT GGG ACT CAC GTT CGG TGA GGG TAC AGC GGA CCT TCG AGC ACG CAA TAT CGT GGG CCG
 (cys gly thr his val arg) OPA (gly tyr ser gly pro ser ser thr gln tyr arg gly pro
 61/21 SEQ ID No. 449 91/31
 GCT GGC AAC CGT CGG TTT CGA CGT TGG TGA CGA CCC CTC GTT CAT GAA TCG TTC TTG AGC
 ala gly asn arg arg phe arg arg trp) OPA (arg pro leu val his glu ser phe leu ser
 121/41 SEQ ID No. 450 151/51
 TCC CCG TTT TGC TGG ATG CCC AGG CAC CGC CGG TAC TGC TGC GCT TAA GCT TGT CGC ACA
 ser pro phe cys trp met pro arg his arg arg tyr cys cys ala) OCH (ala cys arg thr
 181/61 211/71 SEQ ID No. 451
 TGG TGC CGG CAG GGA GGA ACA GTG GGC AAG CAG CTA GCC GCG CTC GCC GCG CTG GTC GGT
 trp cys arg gln gly gly thr val gly lys gln leu ala ala leu ala ala leu val gly
 241/81 271/91
 GCG TGC ATG CTC GCA GCC GGA TGC ACC AAC GTG GTC GAC GGG ACC GCC GTG GCT GCC GAC
 ala cys met leu ala ala gly cys thr asn val val asp gly thr ala val ala ala asp
 301/101
 AAA TCC GGA CCA CTG CAT CAG GAT C
 lys ser gly pro leu his gln asp)

SEQ ID Nos. 447-451

FIGURE 20A'

1/1 31/11
 SEQ ID No. 452 GTG GGA CTC ACG TTC GGT GAG GGT ACA GCG GAC CTT CGA GCA CGC AAT ATC GTG GGC CGG
 (val gly leu thr phe gly glu gly thr ala asp leu arg ala arg asn ile val gly arg
 61/21 91/31
 CTG GCA ACC GTC GGT TTC GAC GTT GGT GAC GAC CCC TCG TTC ATG AAT CGT TCT TGA GCT
 leu ala thr val gly phe asp val gly asp asp pro ser phe met asn arg ser) OPA (ala
 121/41 151/51 SEQ ID No. 454
 CCC CGT TTT GCT GGA TGC CCA GGC ACC GCC GGT ACT GCT GCG CTT AAG CTT GTC GCA CAT
 pro arg phe ala gly cys pro gly thr ala gly thr ala ala leu lys leu val ala his
 181/61 211/71
 GGT GCC GGC AGG GAG GAA CAG TGG GCA AGC AGC TAG CCG CGC TCG CCG CGC TGG TCG GTG
 gly ala gly arg glu glu gln trp ala ser ser) AMB (pro arg ser pro arg trp ser val
 241/81 271/91 SEQ ID No. 455
 CGT GCA TGC TCG CAG CCG GAT GCA CCA ACG TGG TCG ACG GGA CCG CCG TGG CTG CCG ACA
 arg ala cys ser gln pro asp ala pro thr trp ser thr gly pro pro trp leu pro thr
 301/101
 AAT CCG GAC CAC TGC ATC AGG ATC
 asn pro asp his cys ile arg ile)

SEQ ID Nos. 452-455

FIGURE 20B'

1/1 31/11
 20 ID No. 456 GTG TGG GAC TCA CGT TCG GTG AGG GTA CAG CGG ACC TTC GAG CAC GCA ATA TCG TGG GCC
 20 ID No. 457 (val trp asp ser arg ser val arg val gln arg thr phe glu his ala ile ser trp ala
 61/21 91/31
 GGC TGG CAA CCG TCG GTT TCG ACG TTG GTG ACG ACC CCT CGT TCA TGA ATC GTT CTT GAG
 gly trp gln pro ser val ser thr leu val thr thr pro arg ser) OPA (ile val leu glu
 121/41 151/51 SEQ ID No. 458
 CTC CCC GTT TTG CTG GAT GCC CAG GCA CCG CCG GTA CTG CTG CGC TTA AGC TTG TCG CAC
 leu pro val leu leu asp ala gln ala pro pro val leu leu arg leu ser leu ser his
 181/61 211/71
 ATG GTG CCG GCA GGG AGG AAC AGT GGG CAA GCA GCT AGC CGC GCT CGC CGC GCT GGT CGG
 met val pro ala gly arg asn ser gly gln ala ala ser arg ala arg ala gly arg
 241/81 271/91
 TGC GTG CAT GCT CGC AGC CGG ATG CAC CAA CGT GGT CGA CGG GAC CGC CGT GGC TGC CGA
 cys val his ala arg ser arg met his gln arg gly arg arg asp arg arg gly cys arg
 301/101
 CAA ATC CGG ACC ACT GCA TCA GGA TC
 gln ile arg thr thr ala ser gly)

SEQ ID Nos. 456-458

FIGURE 20C'

sequence Rv3576 predicted by Cole et al. (Nature 393:537-544) and containing seq20A'

1/1 31/11
 20 ID No. 459 atg ggc aag cag cta gcc gcg ctc gcc gcg ctg gtc ggt gcg tgc atg ctc gca gcc gga
 20 ID No. 460 (met gly lys gln leu ala ala leu ala ala leu val gly ala cys met leu ala ala gly
 61/21 91/31
 tgc acc aac gtg gtc gac ggg acc gcc gtg gct gcc gac aaa tcc gga cca ctg cat cag
 cys thr asn val val asp gly thr ala val ala ala asp lys ser gly pro leu his gln
 121/41 151/51
 gat ccg ata ccg gtt tca gcg ctt gaa ggg ctg ctt ctc gac ttg agc cag atc aat gcc
 asp pro ile pro val ser ala leu glu gly leu leu leu asp leu ser gln ile asn ala
 181/61 211/71
 gcg ctg ggt gcg aca tcg atg aag gtg tgg ttc aac gcc aag gca atg tgg gac tgg agc
 ala leu gly ala thr ser met lys val trp phe asn ala lys ala met trp asp trp ser
 241/81 271/91
 aag agc gtg gcc gac aag aat tgc ctg gct atc gac ggt cca gca cag gaa aag gtc tat
 lys ser val ala asp lys asn cys leu ala ile asp gly pro ala gln glu lys val tyr
 301/101 331/111
 gcc ggc acc ggg tgg acc gct atg cgc ggc caa cgg ctg gat gac agc atc gat gac tcc
 ala gly thr gly trp thr ala met arg gly gln arg leu asp asp ser ile asp asp ser
 361/121 391/131
 aag aaa cgc gac cac tac gcc att caa gcg gtc gtc ggc ttc ccg acc gca cat gat gcc
 lys lys arg asp his tyr ala ile gln ala val val gly phe pro thr ala his asp ala
 421/141 451/151
 gag gag ttc tac agc tcc tcg gtg caa agc tgg agc agc tgc tcg aac cgc cgg ttt gtc
 glu glu phe tyr ser ser ser val gln ser trp ser ser cys ser asn arg arg phe val
 481/161 511/171
 gaa gtc acc ccc gga cag gac gac gcc gcc tgg act gtg gct gac gtt gtc aac gac aac
 glu val thr pro gly gln asp asp ala ala trp thr val ala asp val val asn asp asn
 541/181 571/191
 ggc atg ctc agt agc tcg cag gtt cag gaa ggc ggc gac gga tgg acc tgc cag cgt gcc
 gly met leu ser ser ser gln val gln glu gly gly asp gly trp thr cys gln arg ala
 601/201 631/211
 ctg act gcg cgc aac aac gtc act atc gac att gtc acg tgc gcc tat agc caa ccg gat
 leu thr ala arg asn asn val thr ile asp ile val thr cys ala tyr ser gln pro asp
 661/221 691/231
 ttg gtg gcg att ggc atc gct aac caa atc gcg gcc aag gtt gct aag cag tag
 leu val ala ile gly ile ala asn gln ile ala ala lys val ala lys gln) AMB

SEQ ID Nos. 459-460

FIGURE 20D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv3576

1/1	31/11
seq ID No. 461 taa gct tgt cgc aca tgg tgc cgg cag gga gga aca gtg ggc aag cag cta gcc gcg ctc	
seq ID No. 462 OCH ala cys arg thr trp cys arg gln gly gly thr val gly lys gln leu ala ala leu	
61/21	91/31
gcc gcg ctg gtc ggt gcg tgc atg ctc gca gcc gga tgc acc aac gtg gtc gac ggg acc	
ala ala leu val gly ala cys met leu ala ala gly cys thr asn val val asp gly thr	
121/41	151/51
gcc gtg gct gcc gac aaa tcc gga cca ctg cat cag gat ccg ata ccg gtt tca gcg ctt	
ala val ala ala asp lys ser gly pro leu his gln asp pro ile pro val ser ala leu	
181/61	211/71
gaa ggg ctg ctt ctc gac ttg agc cag atc aat gcc gcg ctg ggt gcg aca tcg atg aag	
glu gly leu leu leu asp leu ser gln ile asn ala ala leu gly ala thr ser met lys	
241/81	271/91
gtg tgg ttc aac gcc aag gca atg tgg gac tgg agc aag agc gtg gcc gac aag aat tgc	
val trp phe asn ala lys ala met trp asp trp ser lys ser val ala asp lys asn cys	
301/101	331/111
ctg gct atc gac ggt cca gca cag gaa aag gtc tat gcc ggc acc ggg tgg acc gct atg	
leu ala ile asp gly pro ala gln glu lys val tyr ala gly thr gly trp thr ala met	
361/121	391/131
cgc ggc caa cgg ctg gat gac agc atc gat gac tcc aag aaa cgc gac cac tac gcc att	
arg gly gln arg leu asp asp ser ile asp asp ser lys lys arg asp his tyr ala ile	
421/141	451/151
caa gcg gtc gtc ggc ttc ccg acc gca cat gat gcc gag gag ttc tac agc tcc tcg gtg	
gln ala val val gly phe pro thr ala his asp ala glu glu phe tyr ser ser ser val	
481/161	511/171
caa agc tgg agc agc tgc tcg aac cgc cgg ttt gtc gaa gtc acc ccc gga cag gac gac	
gln ser trp ser ser cys ser asn arg arg phe val glu val thr pro gly gln asp asp	
541/181	571/191
gcc gcc tgg act gtg gct gac gtt gtc aac gac aac ggc atg ctc agt agc tcg cag gtt	
ala ala trp thr val ala asp val val asn asp asn gly met leu ser ser ser gln val	
601/201	631/211
cag gaa ggc ggc gac gga tgg acc tgc cag cgt gcc ctg act gcg cgc aac aac gtc act	
gln glu gly gly asp gly trp thr cys gln arg ala leu thr ala arg asn asn val thr	
661/221	691/231
atc gac att gtc acg tgc gcc tat agc caa ccg gat ttg gtg gcg att ggc atc gct aac	
ile asp ile val thr cys ala tyr ser gln pro asp leu val ala ile gly ile ala asn	
721/241	
caa atc gcg gcc aag gtt gct aag cag tag	
gln ile ala ala lys val ala lys gln) AMB	

SEQ ID Nos. 461-462

FIGURE 20F

1/1 31/11
 SEQ ID No. 463 GTC CTG GTC GCC GCG CAA CTG GCC GGT CCC GAT GGA AAG TGT TCA CGA TCG CGC TTC TGC
 SEQ ID No. 464 (val leu val ala ala gln leu ala gly pro asp gly lys cys ser arg ser arg phe cys
 61/21 91/31
 CGC TGG TAG TGG CGA TGG TGT TAG CAG GAT TGC GGG TCG AGG CTG CGA TGG CCA GCA CCA
 arg trp) AMB (trp arg trp cys) AMB (gln asp cys gly ser arg leu arg trp pro ala pro
 121/41 SEQ ID No. 465 151/51
 GCG GCC TGC GGC TGG TCG CCG CGC GCG CCG AAA TGA TAC CCG CGA TCA CGA AAT ACA TGT
 ala ala cys gly trp ser pro arg ala pro lys) OPA (tyr pro arg ser arg asn thr cys
 181/61 211/71 SEQ ID No. 467
 CGG CGC TGG ACG TCG CCG TGC TGG CCA GCT CGA CCG GAC ACG ATG TGG AGG GGG CGC AGA
 arg arg trp thr ser pro cys trp pro ala arg pro asp thr met trp arg gly arg arg
 241/81 271/91
 AAA ACT TCA CCG CCC GCA AGT ACG AGC TGC AGA CGC GAC TGG CCG ACA CCG ACG TCA TCG
 lys thr ser pro pro ala ser thr ser cys arg arg asp trp pro thr pro thr ser ser
 301/101 331/111
 CAG ACG TGC GGT CGG GAG TGA ACA CGC TGC TCA ACG GCG GTC AGG CGC TGC TGG ATA AGA
 gln thr cys gly arg glu) OPA (thr arg cys ser thr ala val arg arg cys trp ile arg
 361/121 SEQ ID No. 468
 TGC TGG CCG ACA GCA TCG GCT TGC GGG ATC
 cys trp pro thr ala ser ala cys gly ile)

SEQ ID Nos. 463-468

FIGURE 21A

32/11
 SEQ ID No. 469 TCC TGG TCG CCG CGC AAC TGG CCG GTC CCG ATG GAA AGT GTT CAC GAT CGC GCT TCT GCC
 SEQ ID No. 470 (ser trp ser pro arg asn trp pro val pro met glu ser val his asp arg ala ser ala
 62/21 92/31
 GCT GGT AGT GGC GAT GGT GTT AGC AGG ATT GCG GGT CGA GGC TGC GAT GGC CAG CAC CAG
 ala gly ser gly asp gly val ser arg ile ala gly arg gly cys asp gly gln his gln
 122/41 152/51
 CGG CCT GCG GCT GGT CGC CGC GCG CGC CGA AAT GAT ACC CGC GAT CAC GAA ATA CAT GTC
 arg pro ala ala gly arg arg ala arg arg asn asp thr arg asp his glu ile his val
 182/61 212/71
 GGC GCT GGA CGT CGC CGT GCT GGC CAG CTC GAC CGG ACA CGA TGT GGA GGG GGC GCA GAA
 gly ala gly arg arg arg ala gly gln leu asp arg thr arg cys gly gly gly ala glu
 242/81 272/91
 AAA CTT CAC CGC CCG CAA GTA CGA GCT GCA GAC GCG ACT GGC CGA CAC CGA CGT CAT CGC
 lys leu his arg pro gln val arg ala ala asp ala thr gly arg his arg arg his arg
 302/101 332/111
 AGA CGT GCG GTC GGG AGT GAA CAC GCT GCT CAA CGG CGG TCA GGC GCT GCT GGA TAA GAT
 arg arg ala val gly ser glu his ala ala gln arg arg ser gly ala ala gly) OCH (asp
 362/121 SEQ ID No. 471
 GCT GGC CGA CAG CAT CGG CTT GCG GGA TC
 ala gly arg gln his arg leu ala gly)

SEQ ID Nos. 469-470

FIGURE 21B

33/11
 50 ID No. 472 CCT GGT CGC CGC GCA ACT GGC CGG TCC CGA TGG AAA GTG TTC ACG ATC GCG CTT CTG CCG
 50 ID No. 473 (pro gly arg arg ala thr gly arg ser arg trp lys val phe thr ile ala leu leu pro
 63/21 93/31
 CTG GTA GTG GCG ATG GTG TTA GCA GGA TTG CGG GTC GAG GCT GCG ATG GCC AGC ACC AGC
 leu val val ala met val leu ala gly leu arg val glu ala ala met ala ser thr ser
 123/41 153/51
 GGC CTG CGG CTG GTC GCC GCG CGC GCC GAA ATG ATA CCC GCG ATC ACG AAA TAC ATG TCG
 gly leu arg leu val ala ala arg ala glu met ile pro ala ile thr lys tyr met ser
 183/61 213/71
 GCG CTG GAC GTC GCC GTG CTG GCC AGC TCG ACC GGA CAC GAT GTG GAG GGG GCG CAG AAA
 ala leu asp val ala val leu ala ser ser thr gly his asp val glu gly ala gln lys
 243/81 273/91
 AAC TTC ACC GCC CGC AAG TAC GAG CTG CAG ACG CGA CTG GCC GAC ACC GAC GTC ATC GCA
 asn phe thr ala arg lys tyr glu leu gln thr arg leu ala asp thr asp val ile ala
 303/101 333/111
 GAC GTG CGG TCG GGA GTG AAC ACG CTG CTC AAC GGC GGT CAG GCG CTG CTG GAT AAG ATG
 asp val arg ser gly val asn thr leu leu asn gly gly gln ala leu leu asp lys met
 363/121
 CTG GCC GAC AGC ATC GGC TTG CGG GAT C
 leu ala asp ser ile gly leu arg asp)

SEQ ID Nos. 472-473

FIGURE 21C

part of the nucleotide sequence of seq21A

1/1 31/11
 50 ID No. 474 ACG ATC GCG CTT CTG CCG CTG GTA GTG GCG ATG GTG TTA GCA GGA TTG CGG GTC GAG GCT
 50 ID No. 475 (thr ile ala leu leu pro leu val val ala met val leu ala gly leu arg val glu ala
 61/21 91/31
 GCG ATG GCC AGC ACC AGC GGC CTG CGG CTG GTC GCC GCG CGC GCC GAA ATG ATA CCC GCG
 ala met ala ser thr ser gly leu arg leu val ala ala arg ala glu met ile pro ala
 121/41 151/51
 ATC ACG AAA TAC ATG TCG GCG CTG GAC GTC GCC GTG CTG GCC AGC TCG ACC GGA CAC GAT
 ile thr lys tyr met ser ala leu asp val ala val leu ala ser ser thr gly his asp
 181/61 211/71
 GTG GAG GGG GCG CAG AAA AAC TTC ACC GCC CGC AAG TAC GAG CTG CAG ACG CGA CTG GCC
 val glu gly ala gln lys asn phe thr ala arg lys tyr glu leu gln thr arg leu ala
 241/81 271/91
 GAC ACC GAC GTC ATC GCA GAC GTG CGG TCG GGA GTG AAC ACG CTG CTC AAC GGC GGT CAG
 asp thr asp val ile ala asp val arg ser gly val asn thr leu leu asn gly gly gln
 301/101 331/111
 GCG CTG CTG GAT AAG ATG CTG GCC GAC AGC ATC GGC TTG CGG GAT C
 ala leu leu asp lys met leu ala asp ser ile gly leu arg asp)

SEQ ID Nos. 474-475

FIGURE 21A'

80/185

EO ID NO. 476 1/1
 EO ID NO. 477 31/11
 CGA TCG CGC TTC TGC CGC TGG TAG TGG CGA TGG TGT TAG CAG GAT TGC GGG TCG AGG CTG
 (arg ser arg phe cys arg trp) AMB (trp arg trp cys) AMB (gln asp cys gly ser arg leu
 61/21
 CGA TGG CCA GCA CCA GCG GCC TGC GGC TGG TCG CCG CGC GCG CCG AAA TGA TAC CCG CGA
 arg trp pro ala pro ala ala cys gly trp ser pro arg ala pro lys) OPA (tyr pro arg
 121/41
 TCA CGA AAT ACA TGT CGG CGC TGG ACG TCG CCG TGC TGG CCA GCT CGA CCG GAC ACG ATG
 ser arg asn thr cys arg arg trp thr ser pro cys trp pro ala arg pro asp thr met
 181/61
 TGG AGG GGG CGC AGA AAA ACT TCA CCG CCC GCA AGT ACG AGC TGC AGA CGC GAC TGG CCG
 trp arg gly arg arg lys thr ser pro pro ala ser thr ser cys arg arg asp trp pro
 241/81
 ACA CCG ACG TCA TCG CAG ACG TGC GGT CGG GAG TGA ACA CGC TGC TCA ACG GCG GTC AGG
 thr pro thr ser ser gln thr cys gly arg glu) OPA (thr arg cys ser thr ala val arg
 301/101
 CGC TGC TGG ATA AGA TGC TGG CCG ACA GCA TCG GCT TGC GGG ATC
 arg cys trp ile arg cys trp pro thr ala ser ala cys gly ile)

SEQ ID Nos. 476-481

FIGURE 21B'

EO ID NO. 482 1/1
 EO ID NO. 483 31/11
 CAC GAT CGC GCT TCT GCC GCT GGT AGT GGC GAT GGT GTT AGC AGG ATT GCG GGT CGA GGC
 (his asp arg ala ser ala ala gly ser gly asp gly val ser arg ile ala gly arg gly
 61/21
 TGC GAT GGC CAG CAC CAG CGG CCT GCG GCT GGT CGC CGC GCG CGC CGA AAT GAT ACC CGC
 cys asp gly gln his gln arg pro ala ala gly arg arg ala arg arg asn asp thr arg
 121/41
 GAT CAC GAA ATA CAT GTC GGC GCT GGA CGT CGC CGT GCT GGC CAG CTC GAC CGG ACA CGA
 asp his glu ile his val gly ala gly arg arg arg ala gly gln leu asp arg thr arg
 181/61
 TGT GGA GGG GGC GCA GAA AAA CTT CAC CGC CCG CAA GTA CGA GCT GCA GAC GCG ACT GGC
 cys gly gly gly ala glu lys leu his arg pro gln val arg ala ala asp ala thr gly
 241/81
 CGA CAC CGA CGT CAT CGC AGA CGT GCG GTC GGG AGT GAA CAC GCT GCT CAA CGG CGG TCA
 arg his arg arg his arg arg arg ala val gly ser glu his ala ala gln arg arg ser
 301/101
 GGC GCT GCT GGA TAA GAT GCT GGC CGA CAG CAT CGG CTT GCG GGA TC
 gly ala ala gly) OCH (asp ala gly arg gln his arg leu ala gly)

SEQ ID NO. 484

SEQ ID Nos. 482-484

FIGURE 21C'

sequence Rv3365c predicted by Cole et al. (Nature 393:537-544) and containing Seq21A'

1/1	31/11
gtg acc atg ttc gcc cgc ccg acc atc ccg	gtc gcg gcg gcc gct tct gat att tcc gcc
(val thr met phe ala arg pro thr ile pro	val ala ala ala ala ser asp ile ser ala
61/21	91/31
ccg gct caa ccg gcc cgc ggc aaa cct cag	caa cgc ccg ccg tcc tgg tcg ccg cgc aac
pro ala gln pro ala arg gly lys pro gln	gln arg pro pro ser trp ser pro arg asn
121/41	151/51
tgg ccg gtc cga tgg aaa gtg ttc acg atc	gcg ctt ctg ccg ctg gta gtg gcg atg gtg
trp pro val arg trp lys val phe thr ile	ala leu leu pro leu val val ala met val
181/61	211/71
tta gca gga ttg ccg gtc gag gct gcg atg	gcc agc acc agc ggc ctg ccg ctg gtc gcc
leu ala gly leu arg val glu ala ala met	ala ser thr ser gly leu arg leu val ala
241/81	271/91
gcg cgc gcc gaa atg ata ccc gcg atc acg	aaa tac atg tcg gcg ctg gac gtc gcc gtg
ala arg ala glu met ile pro ala ile thr	lys tyr met ser ala leu asp val ala val
301/101	331/111
ctg gcc agc tcg acc gga cac gat gtg gag	ggg gcg cag aaa aac ttc acc gcc cgc aag
leu ala ser ser thr gly his asp val glu	gly ala gln lys asn phe thr ala arg lys
361/121	391/131
tac gag ctg cag acg cga ctg gcc gac acc	gac gtc atc gca gac gtg ccg tcg gga gtg
tyr glu leu gln thr arg leu ala asp thr	asp val ile ala asp val arg ser gly val
421/141	451/151
aac acg ctg ctc aac ggc ggt cag gcg ctg	ctg gat aag gtg ctg gcc gac agc atc ggc
asn thr leu leu asn gly gly gln ala leu	leu asp lys val leu ala asp ser ile gly
481/161	511/171
ttg ccg gat ccg gtc acc gcc tac gcg ccg	ctg ctg ttg acg gcc cag aac gtg att gac
leu arg asp arg val thr ala tyr ala pro	leu leu leu thr ala gln asn val ile asp
541/181	571/191
gcg tcg gtg ccg gtt gac agc gag caa atc	cga acc cag gtg cag ggt ttg agc cga gcc
ala ser val arg val asp ser glu gln ile	arg thr gln val gln gly leu ser arg ala
601/201	631/211
gtt ggc gcc cgc ggg cag atg acg atg cag	gag atc ctg gtg act cgc ggc gcc gac ctt
val gly ala arg gly gln met thr met gln	glu ile leu val thr arg gly ala asp leu
661/221	691/231
gcc gag ccg caa ctg cgc agc gcg atg gtt	acc ctg gcc ggc acc gaa ccc tcg acg ctg
ala glu pro gln leu arg ser ala met val	thr leu ala gly thr glu pro ser thr leu
721/241	751/251
ttc ggg atg agc gcg gcg ctc ggt gca ggc	tcg ccg gac acc aag aac ctg cag cag caa
phe gly met ser ala ala leu gly ala gly	ser pro asp thr lys asn leu gln gln gln
781/261	811/271
atg gtg acc agg atg gcg atc atg tcc gat	ccg gcc gtt gca ctg gtc aac aac cca gag
met val thr arg met ala ile met ser asp	pro ala val ala leu val asn asn pro glu
841/281	871/291
ctg ctg cac tcg ata cag atc acc cgc gac	att gcc gag cag gtg atc acc gac acc acc
leu leu his ser ile gln ile thr arg asp	ile ala glu gln val ile thr asp thr thr
901/301	931/311
gag gcg gtg acg aag tcg gtg caa agc cag	gcc acc gac ccg ccg gat gcc gcg att cgc
glu ala val thr lys ser val gln ser gln	ala thr asp arg arg asp ala ala ile arg
961/321	991/331
gac gcc gtg ctg gtg ttg gcc gcc atc gcg	acc gcg atc gtc gtc gtg ttg gtg gtg gcg
asp ala val leu val leu ala ala ile ala	thr ala ile val val val leu val val ala

SEQ ID Nos 485-486

FIGURE 21D

82/185

1021/341	1051/351
cgc acg ctg gtc ggg ccg atg cgg gta ctg	cgt gat ggg gcg ctc aag gtt gct cat acc
arg thr leu val gly pro met arg val leu	arg asp gly ala leu lys val ala his thr
1081/361	1111/371
gat ctc gac ggc gag atc gcg gcg gtc cgc	gcc ggc gac gag ccg atc ccc gag cca ctg
asp leu asp gly glu ile ala ala val arg	ala gly asp glu pro ile pro glu pro leu
1141/381	1171/391
gcg gtg tac acc acc gag gaa atc ggt cag	gtc gcg cat gcg gtc gac gag ctg cac acc
ala val tyr thr thr glu glu ile gly gln	val ala his ala val asp glu leu his thr
1201/401	1231/411
cgg gcc ctg ttg ctg gcc ggc gag gaa acg	cgg ttg cga ctg ctg gtc aac gag atg ttt
arg ala leu leu leu ala gly glu glu thr	arg leu arg leu leu val asn glu met phe
1261/421	1291/431
gag acc atg tcg cgg cgt agc cgt tcc ctg	gtc gac cag cag ctg tcg gtc atc gac caa
glu thr met ser arg arg ser arg ser leu	val asp gln gln leu ser val ile asp gln
1321/441	1351/451
ctg gag cgc aac gag gag gat ccc gcc cga	ctc gac agc ctt ttc cgg ctc gat cac ctg
leu glu arg asn glu glu asp pro ala arg	leu asp ser leu phe arg leu asp his leu
1381/461	1411/471
gcc gcc cgg ctg cgc cgc aac agc gcc aac	ctg ctg gtg ctg gcc ggt gcg cag att acc
ala ala arg leu arg arg asn ser ala asn	leu leu val leu ala gly ala gln ile thr
1441/481	1471/491
cgt gac cac cgc gag ccg gtg ccg ctg tca	acc gtg atc agc gcc gcc gtg tca gag gtc
arg asp his arg glu pro val pro leu ser	thr val ile ser ala ala val ser glu val
1501/501	1531/511
gag gac tat cgc cgc gtc gac atc gcg agg	gta ccc gac tgt gcg gta gtc ggc gca gcg
glu asp tyr arg arg val asp ile ala arg	val pro asp cys ala val val gly ala ala
1561/521	1591/531
gct ggt ggc gtc att cat ctg ctt gcc gag	ctg atc gac aac gcg ttg cgc tac tcg tca
ala gly gly val ile his leu leu ala glu	leu ile asp asn ala leu arg tyr ser ser
1621/541	1651/551
ccg acc aca ccc gtt cgg gtt gcc gcc gca	atc ggc agc gaa ggc agt gtt ctg ctg cga
pro thr thr pro val arg val ala ala ala	ile gly ser glu gly ser val leu leu arg
1681/561	1711/571
atc tcg gat tcc ggc ctg ggc atg acc gat	gcc gat cgg cgg atg gcc aat atg cgg ctg
ile ser asp ser gly leu gly met thr asp	ala asp arg arg met ala asn met arg leu
1741/581	1771/591
cgg gcc ggc ggt gag gtc acc ccg gat agt	gcc cgg cac atg ggt ctg ttc gta gtc ggc
arg ala gly gly glu val thr pro asp ser	ala arg his met gly leu phe val val gly
1801/601	1831/611
cgg ctg gcc ggt cgg cac ggc atc cga gtc	ggg ctg cgc ggt ccg gtg acc ggt gaa cag
arg leu ala gly arg his gly ile arg val	gly leu arg gly pro val thr gly glu gln
1861/621	1891/631
ggc acc ggc acc acc gcc gag gtc tac ctg	ccg cta gcc gtg ctc gag ggg acg gcc cca
gly thr gly thr thr ala glu val tyr leu	pro leu ala val leu glu gly thr ala pro
1921/641	1951/651
gcg cag ccg cca aag ccg cgg gta ttt gcg	atc aag ccg ccg tgt cct gaa ccc gcg gcg
ala gln pro pro lys pro arg val phe ala	ile lys pro pro cys pro glu pro ala ala
1981/661	2011/671
gcc gat ccg acg gac gtt ccc gcc gcc atc	ggg ccg cta cca ccg gtc acg ttg ctc ccg
ala asp pro thr asp val pro ala ala ile	gly pro leu pro pro val thr leu leu pro

SEQ ID nos 485-486 (continued 1)

FIGURE 21D (continued 1)

2041/681	2071/691
cgc cgt acc ccg ggg tcc agt ggc atc gcc	gac gtc ccg gcc cag ccg atg cag cag ccg
arg arg thr pro gly ser ser gly ile ala	asp val pro ala gln pro met gln gln arg
2101/701	2131/711
cgg cgc gag ctg aaa aca ccc tgg tgg gag	gat agg ttt caa cag gag ccc aaa caa ccg
arg arg glu leu lys thr pro trp trp glu	asp arg phe gln gln glu pro lys gln pro
2161/721	2191/731
ccc gca cca gaa ccg cga ccg gcg ccg ccg	ccc gcc aaa ccc gcg cca ccg gcg ggc ccg
pro ala pro glu pro arg pro ala pro pro	pro ala lys pro ala pro pro ala gly pro
2221/741	2251/751
gtt gat gac gac gtc atc tac cgg cgg atg	ctc tcc gag atg gtg ggt gac ccg cac gag
val asp asp asp val ile tyr arg arg met	leu ser glu met val gly asp pro his glu
2281/761	2311/771
ctg gcc cac agc ccc gat ctg gac tgg aag	tcg gtg tgg gac cac ggc tgg tcg gcg gcc
leu ala his ser pro asp leu asp trp lys	ser val trp asp his gly trp ser ala ala
2341/781	2371/791
gcc gag gcc gcg gac aag ccc gtg cag tcc	cgc acg gac tac ggc ctg ccg gtg cgc gaa
ala glu ala ala asp lys pro val gln ser	arg thr asp tyr gly leu pro val arg glu
2401/801	2431/811
ccc ggg gcc ccg tta gtg ccg ggg gcg gcg	gtg cct gag gga ccc gat ccg gag cat ccg
pro gly ala arg leu val pro gly ala ala	val pro glu gly pro asp arg glu his pro
2461/821	2491/831
ggt gca gcg cta gca tcc aac ggc gga ctt	cat ccc ggc cga gcg ccg ccg cac gcg gct
gly ala ala leu ala ser asn gly gly leu	his pro gly arg ala pro arg his ala ala
2521/841	2551/851
gcg gta cgc gac ccc gac gcg gtt cgt gcc	tcc atc agc agc cat ttc ggc ggc gtg cgc
ala val arg asp pro asp ala val arg ala	ser ile ser ser his phe gly gly val arg
2581/861	2611/871
acc ggg ccg tcg cat gcc cgc gag agc agt	cag gga ccc aat cag caa tga
thr gly arg ser his ala arg glu ser ser	gln gly pro asn gln gln)OPA

SEQ ID Nos. 485-486(continued)

FIGURE 21D (continued)

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ORF according to Cole et al. (Nature 393:537-544) and containing Rv3365c

1/1

31/11

50 ID No. 487 taa ggg tgc ggc cgg tgg cac ggc cgc ggc cac gtg acc atg ttc gcc cgc ccg acc atc
 OCH (gly cys gly arg trp his gly arg gly his val thr met phe ala arg pro thr ile
 20 ID No. 488 61/21 91/31
 ccg gtc gcg gcg gcc gct tct gat att tcc gcc ccg gct caa ccg gcc cgc ggc aaa cct
 pro val ala ala ala ala ser asp ile ser ala pro ala gln pro ala arg gly lys pro
 121/41 151/51
 cag caa cgc ccg ccg tcc tgg tgc ccg cgc aac tgg ccg gtc cga tgg aaa gtg ttc acg
 gln gln arg pro pro ser trp ser pro arg asn trp pro val arg trp lys val phe thr
 181/61 211/71
 atc gcg ctt ctg ccg ctg gta gtg gcg atg gtg tta gca gga ttg ccg gtc gag gct gcg
 ile ala leu leu pro leu val val ala met val leu ala gly leu arg val glu ala ala
 241/81 271/91
 atg gcc agc acc agc ggc ctg ccg ctg gtc gcc gcg cgc gcc gaa atg ata ccc gcg atc
 met ala ser thr ser gly leu arg leu val ala ala arg ala glu met ile pro ala ile
 301/101 331/111
 acg aaa tac atg tgc gcg ctg gac gtc gcc gtg ctg gcc agc tgc acc gga cac gat gtg
 thr lys tyr met ser ala leu asp val ala val leu ala ser ser thr gly his asp val
 361/121 391/131
 gag ggg gcg cag aaa aac ttc acc gcc cgc aag tac gag ctg cag acg cga ctg gcc gac
 glu gly ala gln lys asn phe thr ala arg lys tyr glu leu gln thr arg leu ala asp
 421/141 451/151
 acc gac gtc atc gca gac gtg ccg tgc gga gtg aac acg ctg ctc aac ggc ggt cag gcg
 thr asp val ile ala asp val arg ser gly val asn thr leu leu asn gly gly gln ala
 481/161 511/171
 ctg ctg gat aag gtg ctg gcc gac agc atc gcc ttg ccg gat ccg gtc acc gcc tac gcg
 leu leu asp lys val leu ala asp ser ile gly leu arg asp arg val thr ala tyr ala
 541/181 571/191
 ccg ctg ctg ttg acg gcc cag aac gtg att gac gcg tgc gtg ccg gtt gac agc gag caa
 pro leu leu leu thr ala gln asn val ile asp ala ser val arg val asp ser glu gln
 601/201 631/211
 atc cga acc cag gtg cag ggt ttg agc cga gcc gtt ggc gcc cgc ggg cag atg acg atg
 ile arg thr gln val gln gly leu ser arg ala val gly ala arg gly gln met thr met
 661/221 691/231
 cag gag atc ctg gtg act cgc ggc gcc gac ctt gcc gag ccg caa ctg cgc agc gcg atg
 gln glu ile leu val thr arg gly ala asp leu ala glu pro gln leu arg ser ala met
 721/241 751/251
 gtt acc ctg gcc ggc acc gaa ccc tgc acg ctg ttc ggg atg agc gcg gcg ctc ggt gca
 val thr leu ala gly thr glu pro ser thr leu phe gly met ser ala ala leu gly ala
 781/261 811/271
 ggc tgc ccg gac acc aag aac ctg cag cag caa atg gtg acc agg atg gcg atc atg tcc
 gly ser pro asp thr lys asn leu gln gln gln met val thr arg met ala ile met ser
 841/281 871/291
 gat ccg gcc gtt gca ctg gtc aac aac cca gag ctg ctg cac tgc ata cag atc acc cgc
 asp pro ala val ala leu val asn asn pro glu leu leu his ser ile gln ile thr arg

SEQ ID Nos. 487-488

FIGURE 21 E

901/301	931/311
gac att gcc gag cag gtg atc acc gac acc	acc gag gcg gtg acg aag tcg gtg caa agc
asp ile ala glu gln val ile thr asp thr	thr glu ala val thr lys ser val gln ser
961/321	991/331
cag gcc acc gac cgg cgg gat gcc gcg att	cgc gac gcc gtg ctg gtg ttg gcc gcc atc
gln ala thr asp arg arg asp ala ala ile	arg asp ala val leu val leu ala ala ile
1021/341	1051/351
gcg acc gcg atc gtc gtc gtg ttg gtg gtg	gcg gcg acg ctg gtc ggg ccg atg cgg gta
ala thr ala ile val val val leu val val	ala arg thr leu val gly pro met arg val
1081/361	1111/371
ctg cgt gat ggg gcg ctg aag gtt gct cat	acc gat ctg gac ggc gag atc gcg gcg gtc
leu arg asp gly ala leu lys val ala his	thr asp leu asp gly glu ile ala ala val
1141/381	1171/391
cgc gcc ggc gac gag ccg atc ccc gag cca	ctg gcg gtg tac acc acc gag gaa atc ggt
arg ala gly asp glu pro ile pro glu pro	leu ala val tyr thr thr glu glu ile gly
1201/401	1231/411
cag gtc gcg cat gcg gtc gac gag ctg cac	acc cgg gcc ctg ttg ctg gcc ggc gag gaa
gln val ala his ala val asp glu leu his	thr arg ala leu leu leu ala gly glu glu
1261/421	1291/431
acg cgg ttg cga ctg ctg gtc aac gag atg	ttt gag acc atg tcg cgg cgt agc cgt tcc
thr arg leu arg leu leu val asn glu met	phe glu thr met ser arg arg ser arg ser
1321/441	1351/451
ctg gtc gac cag cag ctg tcg gtc atc gac	caa ctg gag gcg aac gag gag gat ccc gcc
leu val asp gln gln leu ser val ile asp	gln leu glu arg asn glu glu asp pro ala
1381/461	1411/471
cga ctg gac agc ctt ttc cgg ctg gat cac	ctg gcc gcc cgg ctg gcg gcg aac agc gcc
arg leu asp ser leu phe arg leu asp his	leu ala ala arg leu arg arg asn ser ala
1441/481	1471/491
aac ctg ctg gtg ctg gcc ggt gcg cag att	acc cgt gac cac gcg gag ccg gtg ccg ctg
asn leu leu val leu ala gly ala gln ile	thr arg asp his arg glu pro val pro leu
1501/501	1531/511
tca acc gtg atc agc gcc gcc gtg tca gag	gtc gag gac tat cgc gcg gtc gac atc gcg
ser thr val ile ser ala ala val ser glu	val glu asp tyr arg arg val asp ile ala
1561/521	1591/531
agg gta ccc gac tgt gcg gta gtc ggc gca	gcg gct ggt ggc gtc att cat ctg ctt gcc
arg val pro asp cys ala val val gly ala	ala ala gly gly val ile his leu leu ala
1621/541	1651/551
gag ctg atc gac aac gcg ttg cgc tac tcg	tca ccg acc aca ccc gtt cgg gtt gcc gcc
glu leu ile asp asn ala leu arg tyr ser	ser pro thr thr pro val arg val ala ala
1681/561	1711/571
gca atc ggc agc gaa ggc agt gtt ctg ctg	cga atc tcg gat tcc ggc ctg ggc atg acc
ala ile gly ser glu gly ser val leu leu	arg ile ser asp ser gly leu gly met thr
1741/581	1771/591
gat gcc gat cgg cgg atg gcc aat atg cgg	ctg cgg gcc ggc ggt gag gtc acc ccg gat
asp ala asp arg arg met ala asn met arg	leu arg ala gly gly glu val thr pro asp
1801/601	1831/611
agt gcc cgg cac atg ggt ctg ttc gta gtc	ggc cgg ctg gcc ggt cgg cac ggc atc cga
ser ala arg his met gly leu phe val val	gly arg leu ala gly arg his gly ile arg

SEQ ID Nos. 487, 488 (continued 1)

FIGURE 21E (continued 1)

1861/621	1891/631
gtc ggg ctg cgc ggt ccg gtg acc ggt gaa	cag ggc acc ggc acc acc gcc gag gtc tac
val gly leu arg gly pro val thr gly glu	gln gly thr gly thr thr ala glu val tyr
1921/641	1951/651
ctg ccg cta gcc gtg ctc gag ggg acg gcc	cca gcg cag ccg cca aag ccg ccg gta ttt
leu pro leu ala val leu glu gly thr ala	pro ala gln pro pro lys pro arg val phe
1981/661	2011/671
gcg atc aag ccg ccg tgt cct gaa ccc gcg	gcg gcc gat ccg acg gac gtt ccc gcc gcc
ala ile lys pro pro cys pro glu pro ala	ala ala asp pro thr asp val pro ala ala
2041/681	2071/691
atc ggg ccg cta cca ccg gtc acg ttg ctc	ccg cgc cgt acc ccg ggg tcc agt ggc atc
ile gly pro leu pro pro val thr leu leu	pro arg arg thr pro gly ser ser gly ile
2101/701	2131/711
gcc gac gtc ccg gcc cag ccg atg cag cag	cgg ccg cgc gag ctg aaa aca ccc tgg tgg
ala asp val pro ala gln pro met gln gln	arg arg arg glu leu lys thr pro trp trp
2161/721	2191/731
gag gat agg ttt caa cag gag ccc aaa caa	ccg ccc gca cca gaa ccg cga ccg gcg ccg
glu asp arg phe gln gln glu pro lys gln	pro pro ala pro glu pro arg pro ala pro
2221/741	2251/751
ccg ccc gcc aaa ccc gcg cca ccg gcg gcc	ccg gtt gat gac gac gtc atc tac cgg ccg
pro pro ala lys pro ala pro pro ala gly	pro val asp asp asp val ile tyr arg arg
2281/761	2311/771
atg ctc tcc gag atg gtg ggt gac ccg cac	gag ctg gcc cac agc ccc gat ctg gac tgg
met leu ser glu met val gly asp pro his	glu leu ala his ser pro asp leu asp trp
2341/781	2371/791
aag tcg gtg tgg gac cac ggc tgg tcg gcg	gcc gcc gag gcc gcg gac aag ccc gtg cag
lys ser val trp asp his gly trp ser ala	ala ala glu ala ala asp lys pro val gln
2401/801	2431/811
tcc cgc acg gac tac ggc ctg ccg gtg cgc	gaa ccc ggg gcc ccg tta gtg ccg ggg gcg
ser arg thr asp tyr gly leu pro val arg	glu pro gly ala arg leu val pro gly ala
2461/821	2491/831
gcg gtg cct gag gga ccc gat ccg gag cat	ccg ggt gca gcg cta gca tcc aac ggc gga
ala val pro glu gly pro asp arg glu his	pro gly ala ala leu ala ser asn gly gly
2521/841	2551/851
ctt cat ccc ggc cga gcg ccg ccg cac gcg	gct gcg gta cgc gac ccc gac gcg gtt cgt
leu his pro gly arg ala pro arg his ala	ala ala val arg asp pro asp ala val arg
2581/861	2611/871
gcc tcc atc agc agc cat ttc ggc ggc gtg	cgc acc ggg ccg tcg cat gcc cgc gag agc
ala ser ile ser ser his phe gly gly val	arg thr gly arg ser his ala arg glu ser
2641/881	
agt cag gga ccc aat cag caa tga	
ser gln gly pro asn gln gln)OPA	

SEQ ID Nos. 487-498 (continued 2)

FIGURE 21E (continued 2)

31/11
 E0 ID No. 489 CTA CGA CAA GGC AAA GGA GCA CAG GGT GAA GCG TGG ACT GAC GGT CGC GGT AGC CGG AGC
 (leu arg gln gly lys gly ala gln gly glu ala trp thr asp gly arg gly ser arg ser
 ID No. 490 61/21 91/31
 CGC CAT TCT GGT CGC AGG TCT TTC CGG ATG TTC AAG CAA CAA GTC GAC TAC AGG AAG CGG
 arg his ser gly arg arg ser phe arg met phe lys gln gln val asp tyr arg lys arg)
 121/41 151/51
 TGA GAC CAC GAC CGC GGC AGG CAC GAC GGC AAG CCC CGG CGC CGC ATC CGG GCC GAA GGT
 OPA (asp his asp arg gly arg his asp gly lys pro arg arg arg ile arg ala glu gly
 ID No. 491 181/61 211/71
 CGT CAT CGA CGG TAA GGA CCA GAA CGT CAC CGG GTC TGT GGT GTG CAC AAC CGC GGC CGG
 arg his arg arg) OCH (gly pro glu arg his arg val cys gly val his asn arg gly arg
 241/81 271/91
 CAA TGT CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC CGT GCT CAC CGA CGG
 gln cys gln his arg asp arg arg gly gly asp arg his cys arg arg ala his arg arg
 301/101 331/111
 CAA CCC TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG CGT CAC GCT GGG ATA
 gln pro ser gly gly glu val arg trp ala arg) OCH (arg gln arg arg his ala gly ile
 361/121 391/131 SEQ ID No. 493
 CAC GTC GGG CAC CGG ACA GGG TAA CGC TCG GCA ACC AAG GAC GGC AGC CAC TAC AAG ATC
 his val gly his arg thr gly) OCH (arg ser ala thr lys asp gly ser his tyr lys ile)
 SEQ ID No. 494

SEQ ID Nos. 489-494

FIGURE 22A

32/11
 E0 ID No. 495 TAC GAC AAG GCA AAG GAG CAC AGG GTG AAG CGT GGA CTG ACG GTC GCG GTA GCC GGA GCC
 (tyr asp lys ala lys glu his arg val lys arg gly leu thr val ala val ala gly ala
 ID No. 496 62/21 92/31
 GCC ATT CTG GTC GCA GGT CTT TCC GGA TGT TCA AGC AAC AAG TCG ACT ACA GGA AGC GGT
 ala ile leu val ala gly leu ser gly cys ser ser asn lys ser thr thr gly ser gly
 122/41 152/51
 GAG ACC ACG ACC GCG GCA GGC ACG ACG GCA AGC CCC GGC GCC GCA TCC GGG CCG AAG GTC
 glu thr thr thr ala ala gly thr thr ala ser pro gly ala ala ser gly pro lys val
 182/61 212/71
 GTC ATC GAC GGT AAG GAC CAG AAC GTC ACC GGG TCT GTG GTG TGC ACA ACC GCG GCC GGC
 val ile asp gly lys asp gln asn val thr gly ser val val cys thr thr ala ala gly
 242/81 272/91
 AAT GTC AAC ATC GCG ATC GGC GGG GCG GCG ACC GGC ATT GCC GCC GTG CTC ACC GAC GGC
 asn val asn ile ala ile gly gly ala ala thr gly ile ala ala val leu thr asp gly
 302/101 332/111
 AAC CCT CCG GAG GTG AAG TCC GTT GGG CTC GGT AAC GTC AAC GGC GTC ACG CTG GGA TAC
 asn pro pro glu val lys ser val gly leu gly asn val asn gly val thr leu gly tyr
 362/121 392/131
 ACG TCG GGC ACC GGA CAG GGT AAC GCT CGG CAA CCA AGG ACG GCA GCC ACT ACA AGA TC
 thr ser gly thr gly gln gly asn ala arg gln pro arg thr ala ala thr thr arg)

SEQ ID Nos. 495-496

FIGURE 22B

33/11
 ED ID No. 497 ACG ACA AGG CAA AGG AGC ACA GGG TGA AGC GTG GAC TGA CGG TCG CGG TAG CCG GAG CCG
 (thr thr arg gln arg ser thr gly) OPA ser val asp OPA arg ser arg AMB (pro glu pro
 ED ID No. 498 63/21 93/31 320 ID No. 499
 CCA TTC TGG TCG CAG GTC TTT CCG GAT GTT CAA GCA ACA AGT CGA CTA CAG GAA GCG GTG
 pro phe trp ser gln val phe pro asp val gln ala thr ser arg leu gln glu ala val
 123/41 153/51
 AGA CCA CGA CCG CGG CAG GCA CGA CGG CAA GCC CCG GCG CCG CAT CCG GGC CGA AGG TCG
 arg pro arg pro arg gln ala arg arg gln ala pro ala pro his pro gly arg arg ser
 183/61 213/71
 TCA TCG ACG GTA AGG ACC AGA ACG TCA CCG GGT CTG TGG TGT GCA CAA CCG CGG CCG GCA
 ser ser thr val arg thr arg thr ser pro gly leu trp cys ala gln pro arg pro ala
 243/81 273/91
 ATG TCA ACA TCG CGA TCG GCG GGG CGG CGA CCG GCA TTG CCG CCG TGC TCA CCG ACG GCA
 met ser thr ser arg ser ala gly arg arg pro ala leu pro pro cys ser pro thr ala
 303/101 333/111
 ACC CTC CGG AGG TGA AGT CCG TTG GGC TCG GTA ACG TCA ACG GCG TCA CGC TGG GAT ACA
 thr leu arg arg) OPA (ser pro leu gly ser val thr ser thr ala ser arg trp asp thr
 363/121 393/131 320 ID No. 500
 CGT CGG GCA CCG GAC AGG GTA ACG CTC GGC AAC CAA GGA CGG CAG CCA CTA CAA GAT C
 arg arg ala pro asp arg val thr leu gly asn gln gly arg gln pro leu gln asp)

SEQ ID Nos. 497-500

FIGURE 22C

31/11
 ED ID No. 501 GCA CAA CCG CGG CCG GCA ATG TCA ACA TCG CGA TCG GCG GGG CGG CGA CCG GCA TTG CCG
 (ala gln pro arg pro ala met ser thr ser arg ser ala gly arg arg pro ala leu pro
 ED ID No. 502 61/21 91/31
 CCG TGC TCA CCG ACG GCA ACC CTC CGG AGG TGA AGT CCG TTG GGC TCG GTA ACG TCA ACG
 pro cys ser pro thr ala thr leu arg arg) OPA (ser pro leu gly ser val thr ser thr
 121/41 151/51 320 ID No. 503
 GCG TCA CGC TGG GAT ACA CGT CGG GCA CCG GAC AGG GTA ACG CCT CGG CAA CCA AGG ACG
 ala ser arg trp asp thr arg arg ala pro asp arg val thr pro arg gln pro arg thr
 181/61 211/71
 GCA GCC ACT ACA AGA TCA CAG GGT GAA GCG TGG ACT GAC GGT CGC GGT AGC CGG AGC CGC
 ala ala thr thr arg ser gln gly glu ala trp thr asp gly arg gly ser arg ser arg
 241/81 271/91
 CAT TCT GGT CGC AGG TCT TTC CGG ATG TTC AAG CAA CAA GTC GAC TAC AGG AAG CGG TGA
 his ser gly arg arg ser phe arg met phe lys gln gln val asp tyr arg lys arg) OPA
 301/101 331/111
 GAC CAC GAC CGC GGC AGG CAC GAC GGC AAG CCC CGG CGC CGC TCC GGG CCG AAG GTC GTC
 (asp his asp arg gly arg his asp gly lys pro arg arg arg ser gly pro lys val val
 ED ID No. 504 361/121 391/131
 ATC GAC GGT AAG GAC CAG AAC GTC ACC GGC TCC GTG GTG TGC ACA ACC GCG GCC GGC AAT
 ile asp gly lys asp gln asn val thr gly ser val val cys thr thr ala ala gly asn
 421/141 451/151
 GTC AAC ATC GCG ATC GGC GGG GCG GCG ACC GGC ATT GCC GCC GTG CTC ACC GAC GGC AAC
 val asn ile ala ile gly gly ala ala thr gly ile ala ala val leu thr asp gly asn
 481/161 511/171
 CCT CCG GAG GTG AAG TCC GTT GGG CTC GGT AAC GTC AAC GGC GTC ACG CTG GGA TAC ACG
 pro pro glu val lys ser val gly leu gly asn val asn gly val thr leu gly tyr thr
 541/181 571/191
 TCG GGC ACC GGA CAG GGT AAC GCC TCG GCA ACC AAG GAC GGC AGC CAC TAC AAG ATC
 ser gly thr gly gln gly asn ala ser ala thr lys asp gly ser his tyr lys ile)

SEQ ID Nos. 501-504

FIGURE 23A

32/11
 50 ID No. 505 CAC AAC CGC GGC CGG CAA TGT CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC
 50 ID No. 506 his asn arg gly arg gln cys gln his arg asp arg arg gly gly asp arg his cys arg
 62/21 92/31
 CGT GCT CAC CGA CGG CAA CCC TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG
 arg ala his arg arg gln pro ser gly gly glu val arg trp ala arg) OCH (arg gln arg
 122/41 152/51
 CGT CAC GCT GGG ATA CAC GTC GGG CAC CGG ACA GGG TAA CGC CTC GGC AAC CAA GGA CGG
 arg his ala gly ile his val gly his arg thr gly) OCH (arg leu gly asn gln gly arg
 182/61 212/71
 CAG CCA CTA CAA GAT CAC AGG GTG AAG CGT GGA CTG ACG GTC GCG GTA GCC GGA GCC GCC
 gln pro leu gln asp his arg val lys arg gly leu thr val ala val ala gly ala ala
 242/81 272/91
 ATT CTG GTC GCA GGT CTT TCC GGA TGT TCA AGC AAC AAG TCG ACT ACA GGA AGC GGT GAG
 ile leu val ala gly leu ser gly cys ser ser asn lys ser thr thr gly ser gly glu
 302/101 332/111
 ACC ACG ACC GCG GCA GGC ACG ACG GCA AGC CCC GGC GCC GCT CCG GGC CGA AGG TCG TCA
 thr thr thr ala ala gly thr thr ala ser pro gly ala ala pro gly arg arg ser ser
 362/121 392/131
 TCG ACG GTA AGG ACC AGA ACG TCA CCG GCT CCG TGG TGT GCA CAA CCG CGG CCG GCA ATG
 ser thr val arg thr arg thr ser pro ala pro trp cys ala gln pro arg pro ala met
 422/141 452/151
 TCA ACA TCG CGA TCG GCG GGG CGG CGA CCG GCA TTG CCG CCG TGC TCA CCG ACG GCA ACC
 ser thr ser arg ser ala gly arg arg pro ala leu pro pro cys ser pro thr ala thr
 482/161 512/171
 CTC CGG AGG TGA AGT CCG TTG GGC TCG GTA ACG TCA ACG GCG TCA CGC TGG GAT ACA CGT
 leu arg arg) OPA (ser pro leu gly ser val thr ser thr ala ser arg trp asp thr arg
 542/181 572/191
 CGG GCA CCG GAC AGG GTA ACG CCT CGG CAA CCA AGG ACG GCA GCC ACT ACA AGA TC
 arg ala pro asp arg val thr pro arg gln pro arg thr ala ala thr thr arg)

SEQ ID Nos. 505-509

FIGURE 23B

33/11
 10 ID No. 510 ACA ACC GCG GCC GGC AAT GTC AAC ATC GCG ATC GGC GGG GCG GCG ACC GGC ATT GCC GCC
 60 ID No. 511 (thr thr ala ala gly asn val asn ile ala ile gly gly ala ala thr gly ile ala ala
 63/21 93/31
 GTG CTC ACC GAC GGC AAC CCT CCG GAG GTG AAG TCC GTT GGG CTC GGT AAC GTC AAC GGC
 val leu thr asp gly asn pro pro glu val lys ser val gly leu gly asn val asn gly
 123/41 153/51
 GTC ACG CTG GGA TAC ACG TCG GGC ACC GGA CAG GGT AAC GCC TCG GCA ACC AAG GAC GGC
 val thr leu gly tyr thr ser gly thr gly gln gly asn ala ser ala thr lys asp gly
 183/61 213/71
 AGC CAC TAC AAG ATC ACA GGG TGA AGC GTG GAC TGA CCG TCG CGG TAG CCG CAG CCG CCA
 ser his tyr lys ile thr gly) OPA ser val asp OPA arg ser arg AMB (pro glu pro pro
 243/81 273/91
 TTC TGG TCG CAG GTC TTT CCG GAT GTT CAA GCA ACA AGT CGA CTA CAG GAA GCG GTG AGA
 phe trp ser gln val phe pro asp val gln ala thr ser arg leu gln glu ala val arg
 303/101 333/111
 CCA CGA CCG CGG CAG GCA CGA CGG CAA GCC CCG GCG CCG CTC CGG GCC GAA GGT CGT CAT
 pro arg pro arg gln ala arg arg gln ala pro ala pro leu arg ala glu gly arg his
 363/121 393/131
 CGA CGG TAA GGA CCA GAA CGT CAC CGG CTC CGT GGT GTG CAC AAC CGC GGC CGG CAA TGT
 arg arg) OCH (gly pro glu arg his arg leu arg gly val his asn arg gly arg gln cys
 423/141 453/151
 CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC CGT GCT CAC CGA CGG CAA CCC
 gln his arg asp arg arg gly gly asp arg his cys arg arg ala his arg arg gln pro
 483/161 513/171
 TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG CGT CAC GCT GGG ATA CAC GTC
 ser gly gly glu val arg trp ala arg) OCH (arg gln arg arg his ala gly ile his val
 543/181 573/191
 GGG CAC CGG ACA GGG TAA CGC CTC GGC AAC CAA GGA CGG CAG CCA CTA CAA GAT C
 gly his arg thr gly) OCH (arg leu gly asn gln gly arg gln pro leu gln asp)
 50 ID No. 515

SEQ ID Nos 510-515

FIGURE 23C

31/11
 30 ID No. 516 CTA ACG ACA GGC AAA GGA GCA CAG GGT GAA GCG TGG ACT GAC GGT CGC GGT AGC CGG AGC
 20 ID No. 517 leu thr thr gly lys gly ala gln gly glu ala trp thr asp gly arg gly ser arg ser
 61/21 91/31
 CGC CAT TCT GGT CGC AGG TCT TTC CGG ATG TTC AAG CAA CAA GTC GAC TAC AGG AAG CGG
 arg his ser gly arg arg ser phe arg met phe lys gln gln val asp tyr arg lys arg)
 121/41 151/51
 TGA GAC CAC GAC CGC GGC AGG CAC GAC GGC AAG CCC CGG CGC CGC TCC GGG CCG AAG GTC
 50 ID No. 518 OPA (asp his asp arg gly arg his asp gly lys pro arg arg arg ser gly pro lys val
 181/61 211/71
 GTC ATC GAC GGT AAG GAC CAG AAC GTC ACC GGC TCC GTG GTG TGC ACA ACC GCG GCC GGC
 val ile asp gly lys asp gln asn val thr gly ser val val cys thr thr ala ala gly
 241/81 271/91
 AAT GTC AAC ATC GCG ATC GGC GGG GCG GCG ACC GGC ATT GCC GCC GTG CTC ACC GAC GGC
 asn val asn ile ala ile gly gly ala ala thr gly ile ala ala val leu thr asp gly
 301/101 331/111
 AAC CCT CCG GAG GTG AAG TCC GTT GGG CTC GGT AAC GTC AAC GGC GTC ACG CTG GGA TAC
 asn pro pro glu val lys ser val gly leu gly asn val asn gly val thr leu gly tyr
 361/121 391/131
 ACG TCG GGC ACC GGA CAG GGT AAC GCC TCG GCA ACC AAG GAC GGC AGC CAC TAC AAG ATC
 thr ser gly thr gly gln gly asn ala ser ala thr lys asp gly ser his tyr lys ile)

SEQ ID Nos. 516-518

FIGURE 24A

32/11
 20 ID No. 519 TAA CGA CAG GCA AAG GAG CAC AGG GTG AAG CGT GGA CTG ACG GTC GCG GTA GCC GGA GCC
 OCH (arg gln ala lys glu his arg val lys arg gly leu thr val ala val ala gly ala
 62/21 92/31
 GCC ATT CTG GTC GCA GGT CTT TCC GGA TGT TCA AGC AAC AAG TCG ACT ACA GGA AGC GGT
 ala ile leu val ala gly leu ser gly cys ser ser asn lys ser thr thr gly ser gly
 122/41 152/51
 GAG ACC ACG ACC GCG GCA GGC ACG ACG GCA AGC CCC GGC GCC GCT CCG GGC CGA AGG TCG
 glu thr thr thr ala ala gly thr thr ala ser pro gly ala ala pro gly arg arg ser
 182/61 212/71
 TCA TCG ACG GTA AGG ACC AGA ACG TCA CCG GCT CCG TGG TGT GCA CAA CCG CGG CCG GCA
 ser ser thr val arg thr arg thr ser pro ala pro trp cys ala gln pro arg pro ala
 242/81 272/91
 ATG TCA ACA TCG CGA TCG GCG GGG CGG CGA CCG GCA TTG CCG CCG TGC TCA CCG ACG GCA
 met ser thr ser arg ser ala gly arg arg pro ala leu pro pro cys ser pro thr ala
 302/101 332/111
 ACC CTC CGG AGG TGA AGT CCG TTG GGC TCG GTA ACG TCA ACG GCG TCA CGC TGG GAT ACA
 thr leu arg arg) OPA (ser pro leu gly ser val thr ser thr ala ser arg trp asp thr
 362/121 392/131
 CGT CGG GCA CCG GAC AGG GTA ACG CCT CGG CAA CCA AGG ACG GCA GCC ACT ACA AGA TC
 arg arg ala pro asp arg val thr pro arg gln pro arg thr ala ala thr thr arg)

SEQ ID Nos. 519-521

FIGURE 24B

33/11
 20 ID No. 522 AAC GAC AGG CAA AGG AGC ACA GGG TGA AGC GTG GAC TGA CGG TCG CGG TAG CCG GAG CCG
 20 ID No. 523 (asn asp arg gln arg ser thr gly) OPA ser val asp OPA arg ser arg AMB (pro glu pro
 63/21 93/31 Seq ID No. 524
 CCA TTC TGG TCG CAG GTC TTT CCG GAT GTT CAA GCA ACA AGT CGA CTA CAG GAA GCG GTG
 pro phe trp ser gln val phe pro asp val gln ala thr ser arg leu gln glu ala val
 123/41 153/51
 AGA CCA CGA CCG CGG CAG GCA CGA CGG CAA GCC CCG GCG CCG CTC CGG GCC GAA GGT CGT
 arg pro arg pro arg gln ala arg arg gln ala pro ala pro leu arg ala glu gly arg
 183/61 213/71
 CAT CGA CGG TAA GGA CCA GAA CGT CAC CGG CTC CGT GGT GTG CAC AAC CGC GGC CGG CAA
 his arg arg) OCH (gly pro glu arg his arg leu arg gly val his asn arg gly arg gln
 243/81 Seq ID No. 525 273/91
 TGT CAA CAT CGC GAT CGG CGG GGC GGC GAC CGG CAT TGC CGC CGT GCT CAC CGA CGG CAA
 cys gln his arg asp arg arg gly gly asp arg his cys arg arg ala his arg arg gln
 303/101 333/111
 CCC TCC GGA GGT GAA GTC CGT TGG GCT CGG TAA CGT CAA CGG CGT CAC GCT GGG ATA CAC
 pro ser gly gly glu val arg trp ala arg) OCH (arg gln arg arg his ala gly ile his
 363/121 393/131 Seq ID No. 526
 GTC GGG CAC CGG ACA GGG TAA CGC CTC GGC AAC CAA GGA CGG CAG CCA CTA CAA GAT C
 val gly his arg thr gly) OCH (arg leu gly asn gln gly arg gln pro leu gln asp)
 Seq ID No. 527

SEQ ID Nos. 522-527

FIGURE 24C

Direct primer

Seq ID No. 528 5' ACG CGG CGC AGC CTG TTG 3'

SEQ ID No. 528

FIGURE 25

Reverse primer

Seq ID No. 529 5' CGA CCT TGG GAT TCG CCT 3'

SEQ ID No. 529

FIGURE 26

31/11
 SEQ ID No. 530 CCT ACC AGC AAG AGC CCA GGG CTT CAC AGG ACC TAA AAG GAG TAG CGC CCA TGG GCT TGA
 pro thr ser lys ser pro gly leu his arg thr) OCH lys glu AMB(arg pro trp ala) OPA
 61/21
 TCC AAT TTT CCT TCC GCC CCG TGC AAT ACC ATC TGC AAG ACC AGC GAC GGC CCG TGG TTG
 (ser asn phe pro ser ala pro cys asn thr ile cys lys thr ser asp gly pro trp leu
 121/41
 CGG TCG CGC AGC TTG CGG AAA CGG GGT ATG GAC CCT GCC GTA CCG TTG TTG CCA CTT GAT
 arg ser arg ser leu arg lys arg gly met asp pro ala val pro leu leu pro leu asp
 181/61
 GTC GTC GCT CTC CAC CCG TCG GGG GGC GAA AGC CAT TCC GAC ACT GGG ATC CTC AAA ACG
 val val ala leu his pro ser gly gly glu ser his ser asp thr gly ile leu lys thr
 241/81
 TCG GCT GAG TGT CTG CAG GGC TCC GGG GAG CAG CCG ATC ATC ACC ATG TAC GAA CTG AAT
 ser ala glu cys leu gln gly ser gly glu gln pro ile ile thr met tyr glu leu asn
 301/101
 AAG TCC CCC CCG CGC GAC TTC CAG ACA TTT GTT GTG GTT TCG GTT GAG GCC GAG GCG AGG
 lys ser pro pro arg asp phe gln thr phe val val val ser val glu ala glu ala arg
 361/121
 CTC ATT TCG CAG CAA GCG GTC TCC GGG TCG CAG CAT CGT TGC GGC GAT CGC GGC GCA GTC
 leu ile ser gln gln ala val ser gly ser gln his arg cys gly asp arg gly ala val
 421/141
 GTC GGA CGA GTC GTC GTC AAC GAC CAC GAT C
 val gly arg val val val asn asp his asp)

SEQ ID Nos. 530-533

FIGURE 27A

31/11
 SEQ ID No. 534 CTA CCA GCA AGA GCC CAG GGC TTC ACA GGA CCT AAA AGG AGT AGC GCC CAT GGG CTT GAT
 leu pro ala arg ala gln gly phe thr gly pro lys arg ser ser ala his gly leu asp
 61/21
 CCA ATT TTC CTT CCG CCC CGT GCA ATA CCA TCT GCA AGA CCA GCG ACG GCC CGT GGT TGC
 pro ile phe leu pro pro arg ala ile pro ser ala arg pro ala thr ala arg gly cys
 121/41
 GGT CGC GCA GCT TGC GGA AAC GGG GTA TGG ACC CTG CCG TAC CGT TGT TGC CAC TTG ATG
 gly arg ala ala cys gly asn gly val trp thr leu pro tyr arg cys cys his leu met
 181/61
 TCG TCG CTC TCC ACC CGT CGG GGG GCG AAA GCC ATT CCG ACA CTG GGA TCC TCA AAA CGT
 ser ser leu ser thr arg arg gly ala lys ala ile pro thr leu gly ser ser lys arg
 241/81
 CGG CTG AGT GTC TGC AGG GCT CCG GGG AGC AGC CGA TCA TCA CCA TGT ACG AAC TGA ATA
 arg leu ser val cys arg ala pro gly ser ser arg ser ser pro cys thr asn) OPA(ile
 301/101
 AGT CCC CCC CGC GCG ACT TCC AGA CAT TTG TTG TGG TTT CGG TTG AGG CCG AGG CGA GGC
 ser pro pro arg ala thr ser arg his leu leu trp phe arg leu arg pro arg arg gly
 361/121
 TCA TTT CGC AGC AAG CGG TCT CCG GGT CGC AGC ATC GTT GCG GCG ATC GCG GCG CAG TCG
 ser phe arg ser lys arg ser pro gly arg ser ile val ala ala ile ala ala gln ser
 421/141
 TCG GAC GAG TCG TCG TCA ACG ACC ACG ATC
 ser asp glu ser ser ser thr thr thr ile)

SEQ ID Nos. 534-536

FIGURE 27B

SEQ ID Nos. 537-541

FIGURE 27C

SEQ ID No. 543

FIGURE 28

SEQ ID No. 644

FIGURE 29

SEQ ID No. 545

MGKQLAALAALVGACMLAAGCTNVVDGTAVAADKSGPLHQDPIPVFTSALEGLLLDLSQINAALGATS
 MKVWFNAKAMWDWSKSVADKNCLAIDGPAQEKVYAGTGFTWTAMRGQRLDDSIDDSKKRDHYAIQAVV
 GFPTAHDAEEFYSSSVQSWSSCSNRRFEVETFTPGQDDAAWTVADVNDNGMLSSSQVQEGGDGWTCC
 RALTARNNVITIDIVTCAYSQPDLVFTAIGIANQIAAKVAKQ

SEQ ID No. 545

FIGURE 30

1/1	31/11
SEQ ID No. 546	AGG CGA ATA CCC GCG AGG GCA GCG CGA CGG CGG CCC TGC CGG CGC CGT GGC TGC TGA ACA
SEQ ID No. 547	(arg arg ile pro ala arg ala ala arg arg arg pro cys arg arg arg gly cys) OPA (thr
61/21	91/31
ACA CAT CCC AGC CGC GCA CGC TTC CGG TAT GCG GCA GGA TAA ACG ACC CCA ACA GCA CGA	SEQ ID No. 548
thr his pro ser arg ala arg phe arg tyr ala ala gly) OCH (thr thr pro thr ala arg	
121/41	151/51
ACA CCA GGA TTG CGA CAA CCA AAG CCC TCG CGC CTG GCT CGA TTT CGC GCG CAA CGC GGC	SEQ ID No. 549
thr pro gly leu arg gln pro lys pro ser arg leu ala arg phe arg ala gln arg gly	
181/61	211/71
GTT CTG CCG CCT CGA TCT CAG CGC GGA GGG CGT CGA GAT C	
val leu pro pro arg ser gln arg gly gly arg arg asp)	

SEQ ID Nos. 546-549

FIGURE 31A

1/1	31/11
SEQ ID No. 550	GGC GAA TAC CCG CGA GGG CAG CGC GAC GGC GGC CCT GCC GGC GCC GTG GCT GCT GAA CAA
SEQ ID No. 551	gly glu tyr pro arg gly gln arg asp gly gly pro ala gly ala val ala ala glu gln
61/21	91/31
CAC ATC CCA GCC GCG CAC GCT TCC GGT ATG CGG CAG GAT AAA CGA CCC CAA CAG CAC GAA	
his ile pro ala ala his ala ser gly met arg gln asp lys arg pro gln gln his glu	
121/41	151/51
CAC CAG GAT TGC GAC AAC CAA AGC CCT CGC GCC TGG CTC GAT TTC GCG CGC AAC GCG GCG	
his gln asp cys asp asn gln ser pro arg ala trp leu asp phe ala arg asn ala ala	
181/61	211/71
TTC TGC CGC CTC GAT CTC AGC GCG GAG GGC GTC GAG ATC	
phe cys arg leu asp leu ser ala glu gly val glu ile)	

SEQ ID Nos. 550-551

FIGURE 31B

96/185

1/1
 31/11
 GCG AAT ACC CGC GAG GGC AGC GCG ACG GCG GCC CTG CCG GCG CCG TGG CTG CTG AAC AAC
 ala asn thr arg glu gly ser ala thr ala ala leu pro ala pro trp leu leu asn asn
 61/21 91/31
 ACA TCC CAG CCG CGC ACG CTT CCG GTA TGC GGC AGG ATA AAC GAC CCC AAC AGC ACG AAC
 thr ser gln pro arg thr leu pro val cys gly arg ile asn asp pro asn ser thr asn
 121/41 151/51
 ACC AGG ATT GCG ACA ACC AAA GCC CTC GCG CCT GGC TCG ATT TCG CGC GCA ACG CGG CGT
 thr arg ile ala thr thr lys ala leu ala pro gly ser ile ser arg ala thr arg arg
 181/61 211/71
 TCT GCC GCC TCG ATC TCA GCG CGG AGG GCG TCG AGA TC
 ser ala ala ser ile ser ala arg arg ala ser arg)

SEQ ID Nos. 552-553

FIGURE 31C

ORF according to Cole et al. (Nature 393:537-544) and containing seq31A

1/1
 31/11
 taa acg acc cca aca gca cga aca cca gga ttg cga caa cca aag ccc tcg cgc ctg gct
 OCH thr thr pro thr ala arg thr pro gly leu arg gln pro lys pro ser arg leu ala
 61/21 91/31
 cga ttt cgc gcg caa cgc ggc gtt ctg ccg cct cga tct cag cgc gga ggg cgt cga gat
 arg phe arg ala gln arg gly val leu pro pro arg ser gln arg gly gly arg arg asp
 121/41 151/51
 ccc cgg cgt cgt gtt cgt ggc tca tca tct gca tcc tcc ggg ctt ggc cgc gct gac cgg
 pro arg arg arg val arg gly ser ser ser ala ser ser gly leu gly arg ala asp arg
 181/61 211/71
 cag ccc gac ccc agg cat gcc cag gcc gac ggc gcg ccc cgg ctg ccc ggc ggt gtg cgc
 gln pro asp pro arg his ala gln ala asp gly ala pro arg leu pro gly gly val arg
 241/81 271/91
 gtc gcc ggc gcg ggt gcg gcg gtg ggt cag gac gcc ggc gtc ggc gat gag gtg gtg cgg
 val ala gly ala gly ala ala val gly gln asp ala gly val gly asp glu val val arg
 301/101 331/111
 cgc cgc ttc ggt gac ctt cgt ggt gat gac gtc gcc ggg acg cac gcg cgg ctg gcc ggc
 arg arg phe gly asp leu arg gly asp asp val ala gly thr his ala arg leu ala gly
 361/121 391/131
 ggt gaa gtg cac cag gcg ccc gtc gcg cgc ccg ccc gct cat gcg cgc cgt gac ggt gtc
 gly glu val his gln ala pro val ala arg pro pro ala his ala arg arg asp gly val
 421/141 451/151
 ctt gcg ccc ttc ccc ggt ggc cac cag cac ctc gac ggc ctg ccc gac cag ggc gcg gtt
 leu ala pro phe pro gly gly his gln his leu asp gly leu pro asp gln gly ala val
 481/161 511/171
 ggc ttc cag cga gat ttg ctc ctg cag gcg gat cag gcg ttc ata gcg ttc ctg cac aac
 gly phe gln arg asp leu leu leu gln arg asp gln ala phe ile ala phe leu his asn
 541/181 571/191
 ggc ttt cgg cag ctg tcc gtc gag ttg cgc ggc cgg tgt ccc ggg ccg ctt gga gta ttg
 gly phe arg gln leu ser val glu leu arg gly arg cys pro gly pro leu gly val leu
 601/201 631/211
 gaa ggt aaa tgc ggc cgc gaa gcg ggc ccg gcg cac cac gtc gag cgt ggc cgc gaa gtc
 glu gly lys cys gly arg glu ala gly pro ala his his val glu arg gly arg glu val
 661/221 691/231
 ctc ttc ggt ctc ccc ggg gaa acc gac gat cag atc ggt ggt aat cgc ggc atg cgg gat
 leu phe gly leu pro gly glu thr asp asp gln ile gly gly asn arg gly met arg asp
 721/241 751/251
 ggc cgc ccg cac gcg ctc gat gat gcc gag gta gcg ctc ggc acg ata gga ccg ccg cat
 gly arg pro his ala leu asp asp ala glu val ala leu gly thr ile gly pro pro his
 781/261 811/271
 cgc gcg cag gat ccg gtc gga tcc gga ctg tag
 arg ala gln asp pro val gly ser gly leu)AMB

SEQ ID Nos. 554-555

FIGURE 31D

97/185

1/1	31/11
seq ID No. 556	
aga ctg gtg tac acg gag acc aag ctg aac	tcg gca ttc tcc ttc ggc ggg cct aag tgt
seq ID No. 557	
arg leu val tyr thr glu thr lys leu asn	ser ala phe ser phe gly gly pro lys cys
61/21	91/31
cta gtg aag gtc att cag aaa ctg tcg ggc	ttg agc atc aac cgg ttc atc gcg att gac
leu val lys val ile gln lys leu ser gly	leu ser ile asn arg phe ile ala ile asp
121/41	151/51
ttc gtc ggt ttc gcg cgg atg gtc gag gcc	ctc ggc ggc gtc gag gta tgc agc acc acc
phe val gly phe ala arg met val glu ala	leu gly gly val glu val cys ser thr thr
181/61	211/71
ccg ttg cgg gac tac gaa ctg ggc acg gtg	ctg gag cac gcc gga cgc cag gtc att gac
pro leu arg asp tyr glu leu gly thr val	leu glu his ala gly arg gln val ile asp
241/81	271/91
ggg ccg acc gcg ctg aac tat gtg cgc gct	cgc cag gtc acc acc gag agc aat ggc gac
gly pro thr ala leu asn tyr val arg ala	arg gln val thr thr glu ser asn gly asp
301/101	331/111
tac ggg cgc atc aaa cgc cag cag ttg ttt	ttg tcg tcg ctg ctg cgt tcg atg atc
tyr gly arg ile lys arg gln gln leu phe	leu ser ser leu leu arg ser met ile)

SEQ ID Nos. 556-557

FIGURE 32A

1/1	31/11
seq ID No. 558	
gac tgg tgt aca cgg aga cca agc tga act cgg cat tct cct tcg gcg ggc cta agt gtc	
seq ID No. 559	
(asp trp cys thr arg arg pro ser) OPA (thr arg his ser pro ser ala gly leu ser val)	
61/21	seq ID No. 560 91/31
tag tga agg tca ttc aga aac tgt cgg gct tga gca tca acc ggt tca tcg cga ttg act	
AMB OPA (arg ser phe arg asn cys arg ala) OPA (ala ser thr gly ser ser arg leu thr	
121/41	seq ID No. 561 151/51 seq ID No. 562
tcg tcg gtt tcg cgc gga tgg tcg agg ccc tcg gcg gcg tcg agg tat gca gca cca ccc	
ser ser val ser arg gly trp ser arg pro ser ala ala ser arg tyr ala ala pro pro	
181/61	211/71
cgt tgc ggg act acg aac tgg gca cgg tgc tgg agc acg ccg gac gcc agg tca ttg acg	
arg cys gly thr thr asn trp ala arg cys trp ser thr pro asp ala arg ser leu thr	
241/81	271/91
ggc cga ccg cgc tga act atg tgc gcg ctc gcc agg tca cca ccg aga gca atg gcg act	
gly arg pro arg) OPA (thr met cys ala leu ala arg ser pro pro arg ala met ala thr	
301/101	seq ID No. 563 331/111
acg ggc gca tca aac gcc agc agt tgt ttt tgt cgt cgc tgc tgc gtt cga tga tc	
thr gly ala ser asn ala ser ser cys phe cys arg arg cys cys val arg) OPA	

SEQ ID Nos. 558-563

FIGURE 32B

1/1 31/11
 2D ID No. 564 act ggt gta cac gga gac caa gct gaa ctc ggc att ctc ctt cgg cgg gcc taa gtg tct
 Q ID No. 565 (thr gly val his gly asp gln ala glu leu gly ile leu leu arg arg ala) OCH (val ser
 61/21 91/31 SEQ ID No. 566
 agt gaa ggt cat tca gaa act gtc ggg ctt gag cat caa ccg gtt cat cgc gat tga ctt
 ser glu gly his ser glu thr val gly leu glu his gln pro val his arg asp) OPA (leu
 121/41 151/51 SEQ ID No. 567
 cgt cgg ttt cgc gcg gat ggt cga ggc cct cgg cgg cgt cga ggt atg cag cac cac ccc
 arg arg phe arg ala asp gly arg gly pro arg arg arg arg gly met gln his his pro
 181/61 211/71
 gtt gcg gga cta cga act ggg cac ggt gct gga gca cgc cgg acg cca ggt cat tga cgg
 val ala gly leu arg thr gly his gly ala gly ala arg arg thr pro gly his) OPA (arg
 241/81 271/91 SEQ ID No. 568
 gcc gac cgc gct gaa cta tgt gcg cgc tcg cca ggt cac cac cga gag caa tgg cga cta
 ala asp arg ala glu leu cys ala arg ser pro gly his his arg glu gln trp arg leu
 301/101 331/111
 cgg gcg cat caa acg cca gca gtt gtt ttt gtc gtc gct gct gcg ttc gat gat c
 arg ala his gln thr pro ala val val phe val val ala ala ala phe asp asp)

SEQ ID Nos. 564-568

FIGURE 32C

sequence Rv0822c predicted by Cole et al. (Nature 393:537-544) and containing seq 32A

1/1 31/11
 2D ID No. 569 atg agt gac ggc gag agc gcc gcg ccg tgg gca cgg ctc tcc gag tca gca ttc ccc gat
 SEQ ID No. 570 (Met ser asp gly glu ser ala ala pro trp ala arg leu ser glu ser ala phe pro asp
 61/21 91/31
 ggt gtt gac cga tgg atc acg gta ccg ccc gcc aca tgg gtg gca gcc cag ggt ccg cgg
 gly val asp arg trp ile thr val pro pro ala thr trp val ala ala gln gly pro arg
 121/41 151/51
 gac acc cag aat gtc ggc tgt cat gcc acc ggc gcc gtt agt gtg gcc gat ctg atc gcc
 asp thr gln asn val gly cys his ala thr gly ala val ser val ala asp leu ile ala
 181/61 211/71
 agg ctc ggc ccc gct ttt cct gac ctc ccc acg cac cgc cat gtc gcc ccc gaa ccc gag
 arg leu gly pro ala phe pro asp leu pro thr his arg his val ala pro glu pro glu
 241/81 271/91
 cca tcc ggc cgc ggc ccg aag gtc cac gac gac gcc gac gac cag cag gac acc gag gct
 pro ser gly arg gly pro lys val his asp asp ala asp asp gln gln asp thr glu ala
 301/101 331/111
 atc gcc atc ccg gcc cac tcg ctc gag ttc ctc tcg gag ctt ccc gac ctc cgg gca gcc
 ile ala ile pro ala his ser leu glu phe leu ser glu leu pro asp leu arg ala ala
 361/121 391/131
 aac tat ccg cgc gcc gac cac gcc cgc cgt gaa ccc gag cta ccc gcc aag cag cta acc
 asn tyr pro arg ala asp his ala arg arg glu pro glu leu pro gly lys gln leu thr
 421/141 451/151
 gga tcg gct cga gtg cgg cca ttg cgg atc cgc cga acg tcg ccc gcg ccc gcc aag cca
 gly ser ala arg val arg pro leu arg ile arg arg thr ser pro ala pro ala lys pro
 481/161 511/171
 gcg ccg aac tcc ggc cgg cgc ccg atg gtg ctg gcc gcg cgc tcg ctg gcg gct ctg ttt
 ala pro asn ser gly arg arg pro met val leu ala ala arg ser leu ala ala leu phe
 541/181 571/191
 gcc gct ctg gcg ttg gcg ctg acc ggc ggg gca tgg cag tgg agc gcg tcg aag aac agc
 ala ala leu ala leu ala leu thr gly gly ala trp gln trp ser ala ser lys asn ser
 601/201 631/211
 cgg ctg aac atg gta agc gcg ctc gac ccg cat tcg ggc gac atc gtc aac ccc agc ggg
 arg leu asn met val ser ala leu asp pro his ser gly asp ile val asn pro ser gly

SEQ ID Nos. 569-570

FIGURE 32D

661/221	691/231
cag cat ggc gac gag aac ttc ttg ctc gtc	ggt atg gac tct cgt gcc ggg gcg aac gcc
gln his gly asp glu asn phe leu leu val	gly met asp ser arg ala gly ala asn ala
721/241	751/251
aat atc ggc gcc ggc gac gcc gag gac gcc	ggc ggc gca cgt tcg gac acc gtc atg ctg
asn ile gly ala gly asp ala glu asp ala	gly gly ala arg ser asp thr val met leu
781/261	811/271
gtc aac att ccg gcc agc cgc gag cgg gtc	gtc gcg gtg tcg ttc ccc cgc gac ctg gcg
val asn ile pro ala ser arg glu arg val	val ala val ser phe pro arg asp leu ala
841/281	871/291
atc act cca atc caa tgc gag gcg tgg aac	ccc gag acc ggt aag tac gga ccc atc tac
ile thr pro ile gln cys glu ala trp asn	pro glu thr gly lys tyr gly pro ile tyr
901/301	931/311
gac gag aag acg gga acg atg ggt ccc aga	ctg gtg tac acg gag acc aag ctg aac tcg
asp glu lys thr gly thr met gly pro arg	leu val tyr thr glu thr lys leu asn ser
961/321	991/331
gca ttc tcc ttc ggc ggg cct aag tgt cta	gtg aag gtc att cag aaa ctg tcg ggc ttg
ala phe ser phe gly gly pro lys cys leu	val lys val ile gln lys leu ser gly leu
1021/341	1051/351
agc atc aac ccg ttc atc gcg att gac ttc	gtc ggt ttc gcg ccg atg gtc gag gcc ctc
ser ile asn arg phe ile ala ile asp phe	val gly phe ala arg met val glu ala leu
1081/361	1111/371
ggc ggc gtc gag gta tgc agc acc acc ccg	ttg ccg gac tac gaa ctg ggc acg gtg ctg
gly gly val glu val cys ser thr thr pro	leu arg asp tyr glu leu gly thr val leu
1141/381	1171/391
gag cac gcc gga cgc cag gtc att gac ggg	ccg acc gcg ctg aac tat gtg cgc gct cgc
glu his ala gly arg gln val ile asp gly	pro thr ala leu asn tyr val arg ala arg
1201/401	1231/411
cag gtc acc acc gag agc aat ggc gac tac	ggg cgc atc aaa cgc cag cag ttg ttt ttg
gln val thr thr glu ser asn gly asp tyr	gly arg ile lys arg gln gln leu phe leu
1261/421	1291/431
tcg tcg ctg ctg cgt tcg atg atc tcg acg	gac acc ttg ttc aac ctc agc agg ctc aac
ser ser leu leu arg ser met ile ser thr	asp thr leu phe asn leu ser arg leu asn
1321/441	1351/451
aac gtc gtc aac atg ttc atc ggt aac agc	tac gtg gac aac gtc aag acc aaa gac ctg
asn val val asn met phe ile gly asn ser	tyr val asp asn val lys thr lys asp leu
1381/461	1411/471
gtc gaa ctc ggt cga tcg ttg cag cat atg	gcg gcc ggg cac gtc acg ttc gtg acc gtt
val glu leu gly arg ser leu gln his met	ala ala gly his val thr phe val thr val
1441/481	1471/491
ccg acc ggt ata acc gac cag aac ggc gac	gag ccc ccg cgt acc tcc gac atg aag gcg
pro thr gly ile thr asp gln asn gly asp	glu pro pro arg thr ser asp met lys ala
1501/501	1531/511
ctt ttc acc gcc atc atc gac gac gat ccg	ctg ccc ctg gaa aac gat cac aac gcc cag
leu phe thr ala ile ile asp asp asp pro	leu pro leu glu asn asp his asn ala gln
1561/521	1591/531
cgt ctg ggc aac acg ccg tcg acc ccg ccg	acc acc acc aag aag gcg ccg cag gcg ggt
arg leu gly asn thr pro ser thr pro pro	thr thr thr lys lys ala pro gln ala gly
1621/541	1651/551
ctg acc aac gag att cag cac cag cag gtt	acg acg acc tcg cca aaa gag gtc aca gtg
leu thr asn glu ile gln his gln gln val	thr thr thr ser pro lys glu val thr val
1681/561	1711/571
cag gtc tct aac tcg acc ggc cag gcc ggt	ttg gcc acc acc gcc acc gat cag ctc aag
gln val ser asn ser thr gly gln ala gly	leu ala thr thr ala thr asp gln leu lys
1741/581	1771/591
ccg aac ggc ttc aac gtg atg gct ccg gac	gac tac ccg agt tcg ctg ctg gcc acc aca
arg asn gly phe asn val met ala pro asp	asp tyr pro ser ser leu leu ala thr thr
1801/601	1831/611
gtg ttt ttt tcg ccc ggc aac gaa cag gct	gcc gcc acc gtg gcc gcc gtg ttc ggc cag
val phe phe ser pro gly asn glu gln ala	ala ala thr val ala ala val phe gly gln
1861/621	1891/631
tca aag atc gag ccg gtg acc ggg atc ggc	caa ctg gtc cag gtg gtg ctg ggc caa gac
ser lys ile glu arg val thr gly ile gly	gln leu val gln val val leu gly gln asp

100/185

1921/641	1951/651
ttc agc gcg gtg cgc gct ccc ctg ccg agt ggc tcc acc gtc agc gtg cag ata agc cgc	
phe ser ala val arg ala pro leu pro ser gly ser thr val ser val gln ile ser arg	
1981/661	2011/671
aac tcc tcc agc cca ccg acc aag ctg ccc gag gac ctg acg gtc acc aac gcc gcc gac	
asn ser ser ser pro pro thr lys leu pro glu asp leu thr val thr asn ala ala asp	
2041/681	
acc acc tgc gag tag	
thr thr cys glu)AMB	

SEQ ID Nos 569-570(continued 2)
FIGURE 32D (continued 2)

ORF according to Cole et al. (Nature 393:537-544) and containing Rv0822c

1/1	31/11
tag gac atg agt gac ggc gag agc gcc gcg ccg tgg gca cgg ctc tcc gag tca gca ttc	
AMB(asp met ser asp gly glu ser ala ala pro trp ala arg leu ser glu ser ala phe	
61/21	91/31
ccc gat ggt gtt gac cga tgg atc acg gta ccg ccc gcc aca tgg gtg gca gcc cag ggt	
pro asp gly val asp arg trp ile thr val pro pro ala thr trp val ala ala gln gly	
121/41	151/51
ccg cgg gac acc cag aat gtc ggc tgt cat gcc acc gcc gcc gtt agt gtg gcc gat ctg	
pro arg asp thr gln asn val gly cys his ala thr gly ala val ser val ala asp leu	
181/61	211/71
atc gcc agg ctc ggc ccc gct ttt cct gac ctc ccc acg cac cgc cat gtc gcc ccc gaa	
ile ala arg leu gly pro ala phe pro asp leu pro thr his arg his val ala pro glu	
241/81	271/91
ccc gag cca tcc ggc cgc ggc ccg aag gtc cac gac gac gcc gac gac cag cag gac acc	
pro glu pro ser gly arg gly pro lys val his asp asp ala asp asp gln gln asp thr	
301/101	331/111
gag gct atc gcc atc ccg gcc cac tcg ctc gag ttc ctc tcg gag ctt ccc gac ctc cgg	
glu ala ile ala ile pro ala his ser leu glu phe leu ser glu leu pro asp leu arg	
361/121	391/131
gca gcc aac tat ccg cgc gcc gac cac gcc cgc cgt gaa ccc gag cta ccc ggc aag cag	
ala ala asn tyr pro arg ala asp his ala arg arg glu pro glu leu pro gly lys gln	
421/141	451/151
cta acc gga tcg gct cga gtg cgg cca ttg cgg atc cgc cga acg tcg ccc gcg ccc gcc	
leu thr gly ser ala arg val arg pro leu arg ile arg arg thr ser pro ala pro ala	
481/161	511/171
aag cca gcg ccg aac tcc ggc cgg cgc ccg atg gtg ctg gcc gcg cgc tcg ctg gcg gct	
lys pro ala pro asn ser gly arg arg pro met val leu ala ala arg ser leu ala ala	
541/181	571/191
ctg ttt gcc gct ctg gcg ttg gcg ctg acc ggc ggg gca tgg cag tgg agc gcg tcg aag	
leu phe ala ala leu ala leu ala leu thr gly gly ala trp gln trp ser ala ser lys	
601/201	631/211
aac agc cgg ctg aac atg gta agc gcg ctc gac ccg cat tcg ggc gac atc gtc aac ccc	
asn ser arg leu asn met val ser ala leu asp pro his ser gly asp ile val asn pro	
661/221	691/231
agc ggg cag cat ggc gac gag aac ttc ttg ctc gtc ggt atg gac tct cgt gcc ggg gcg	
ser gly gln his gly asp glu asn phe leu leu val gly met asp ser arg ala gly ala	
721/241	751/251
aac gcc aat atc ggc gcc ggc gac gcc gag gac gcc ggc ggc gca cgt tcg gac acc gtc	
asn ala asn ile gly ala gly asp ala glu asp ala gly gly ala arg ser asp thr val	
781/261	811/271
atg ctg gtc aac att ccg gcc agc cgc gag cgg gtc gtc gcg gtg tcg ttc ccc cgc gac	
met leu val asn ile pro ala ser arg glu arg val val ala val ser phe pro arg asp	

SEQ ID Nos. 571-572

FIGURE 32E

841/281	871/291
ctg gcg atc act cca atc caa tgc gag gcg	tgg aac ccc gag acc ggt aag tac gga ccc
leu ala ile thr pro ile gln cys glu ala	trp asn pro glu thr gly lys tyr gly pro
901/301	931/311
atc tac gac gag aag acg gga acg atg ggt	ccc aga ctg gtg tac acg gag acc aag ctg
ile tyr asp glu lys thr gly thr met gly	pro arg leu val tyr thr glu thr lys leu
961/321	991/331
aac tcg gca ttc tcc ttc ggc ggg cct aag	tgt cta gtg aag gtc att cag aaa ctg tcg
asn ser ala phe ser phe gly gly pro lys	cys leu val lys val ile gln lys leu ser
1021/341	1051/351
ggc ttg agc atc aac cgg ttc atc gcg att	gac ttc gtc ggt ttc gcg cgg atg gtc gag
gly leu ser ile asn arg phe ile ala ile	asp phe val gly phe ala arg met val glu
1081/361	1111/371
gcc ctg ggc ggc gtc gag gta tgc agc acc	acc ccg ttg cgg gac tac gaa ctg ggc acg
ala leu gly gly val glu val cys ser thr	thr pro leu arg asp tyr glu leu gly thr
1141/381	1171/391
gtg ctg gag cac gcc gga cgc cag gtc att	gac ggg ccg acc gcg ctg aac tat gtg cgc
val leu glu his ala gly arg gln val ile	asp gly pro thr ala leu asn tyr val arg
1201/401	1231/411
gct cgc cag gtc acc acc gag agc aat ggc	gac tac ggg cgc atc aaa cgc cag cag ttg
ala arg gln val thr thr glu ser asn gly	asp tyr gly arg ile lys arg gln gln leu
1261/421	1291/431
ttt ttg tcg tcg ctg ctg cgt tcg atg atc	tcg acg gac acc ttg ttc aac ctc agc agg
phe leu ser ser leu leu arg ser met ile	ser thr asp thr leu phe asn leu ser arg
1321/441	1351/451
ctc aac aac gtc gtc aac atg ttc atc ggt	aac agc tac gtg gac aac gtc aag acc aaa
leu asn asn val val asn met phe ile gly	asn ser tyr val asp asn val lys thr lys
1381/461	1411/471
gac ctg gtc gaa ctc ggt cga tcg ttg cag	cat atg gcg gcc ggg cac gtc acg ttc gtg
asp leu val glu leu gly arg ser leu gln	his met ala ala gly his val thr phe val
1441/481	1471/491
acc gtt ccg acc ggt ata acc gac cag aac	ggc gac gag ccc ccg cgt acc tcc gac atg
thr val pro thr gly ile thr asp gln asn	gly asp glu pro pro arg thr ser asp met
1501/501	1531/511
aag gcg ctt ttc acc gcc atc atc gac gac	gat ccg ctg ccc ctg gaa aac gat cac aac
lys ala leu phe thr ala ile ile asp asp	asp pro leu pro leu glu asn asp his asn
1561/521	1591/531
gcc cag cgt ctg ggc aac acg ccg tcg acc	ccg ccg acc acc acc aag aag gcg ccg cag
ala gln arg leu gly asn thr pro ser thr	pro pro thr thr thr lys lys ala pro gln
1621/541	1651/551
gcg ggt ctg acc aac gag att cag cac cag	cag gtt acg acg acc tcg cca aaa gag gtc
ala gly leu thr asn glu ile gln his gln	gln val thr thr thr ser pro lys glu val
1681/561	1711/571
aca gtg cag gtc tct aac tcg acc ggc cag	gcc ggt ttg gcc acc acc gcc acc gat cag
thr val gln val ser asn ser thr gly gln	ala gly leu ala thr thr ala thr asp gln
1741/581	1771/591
ctc aag ccg aac ggc ttc aac gtg atg gct	ccg gac gac tac ccg agt tcg ctg ctg gcc
leu lys arg asn gly phe asn val met ala	pro asp asp tyr pro ser ser leu leu ala
1801/601	1831/611
acc aca gtg ttt ttt tcg ccc ggc aac gaa	cag gct gcc gcc acc gtg gcc gcc gtg ttc
thr thr val phe phe ser pro gly asn glu	gln ala ala ala thr val ala ala val phe
1861/621	1891/631
ggc cag tca aag atc gag ccg gtg acc ggg	atc ggc caa ctg gtc cag gtg gtg ctg ggc
gly gln ser lys ile glu arg val thr gly	ile gly gln leu val gln val val leu gly
1921/641	1951/651
caa gac ttc agc gcg gtg cgc gct ccc ctg	ccg agt ggc tcc acc gtc agc gtg cag ata
gln asp phe ser ala val arg ala pro leu	pro ser gly ser thr val ser val gln ile
1981/661	2011/671
agc cgc aac tcc tcc agc cca ccg acc aag	ctg ccc gag gac ctg acg gtc acc aac gcc
ser arg asn ser ser ser pro pro thr lys	leu pro glu asp leu thr val thr asn ala
2041/681	
gcc gac acc acc tgc gag tag	
ala asp thr thr cys glu)AMB	

102/185

SEQ ID NO: 573
SEQ ID NO: 574

1/1 31/11
(CGT CAC CTC TGC CAT GGT CCA TCT ACG GTA TCT GCG ACA AGG GCA GCG TCG ATC CCT CGA
arg his leu cys his gly pro ser thr val ser ala thr arg ala ala ser ile pro arg
61/21 91/31
CAT GCA GAG TCG GTG TTC GCT TCA CGC GAA CTA GGC GCG CCT AGC CTG GAC GAG TCC CCG
his ala glu ser val phe ala ser arg glu leu gly ala pro ser leu asp glu ser pro
121/41 151/51
GGC CGA CAT TCG CCC GAG GCC TTG GCC TCC ATC ACC TAA TTG TGT GCA AAA CCG TAT CTA
gly arg his ser pro glu ala leu ala ser ile thr) OCH (leu cys ala lys pro tyr leu
181/61 211/71
ATT GAT ACG ATT GCG CAC ATG GCT ATC TGG GAT C
ile asp thr ile ala his met ala ile trp asp)

SEQ ID NO: 575

SEQ ID NOS: 573-575

FIGURE 33A

SEQ ID NO: 576

1/1 31/11
(GTC ACC TCT GCC ATG GTC CAT CTA CGG TAT CTG CGA CAA GGG CAG CGT CGA TCC CTC GAC
val thr ser ala met val his leu arg tyr leu arg gln gly gln arg arg ser leu asp
61/21 91/31
ATG CAG AGT CGG TGT TCG CTT CAC GCG AAC TAG GCG CGC CTA GCC TGG ACG AGT CCC CGG
met gln ser arg cys ser leu his ala asn) AMB (ala arg leu ala trp thr ser pro arg
121/41 151/51
GCC GAC ATT CGC CCG AGG CCT TGG CCT CCA TCA CCT AAT TGT GTG CAA AAC CGT ATC TAA
ala asp ile arg pro arg pro trp pro pro ser pro asn cys val gln asn arg ile) OCH
181/61 211/71
TTG ATA CGA TTG CGC ACA TGG CTA TCT GGG ATC
(leu ile arg leu arg thr trp leu ser gly ile)

SEQ ID NO: 579

SEQ ID NOS: 576-579

FIGURE 33B

SEQ ID NO: 580

1/1 31/11
(CCG TCA CCT CTG CCA TGG TCC ATC TAC GGT ATC TGC GAC AAG GGC AGC GTC GAT CCC TCG
pro ser pro leu pro trp ser ile tyr gly ile cys asp lys gly ser val asp pro ser
61/21 91/31
ACA TGC AGA GTC GGT GTT CGC TTC ACG CGA ACT AGG CGC GCC TAG CCT GGA CGA GTC CCC
thr cys arg val gly val arg phe thr arg thr arg arg ala) AMB (pro gly arg val pro
121/41 151/51
GGG CCG ACA TTC GCC CGA GGC CTT GGC CTC CAT CAC CTA ATT GTG TGC AAA ACC GTA TCT
gly pro thr phe ala arg gly leu gly leu his his leu ile val cys lys thr val ser
181/61 211/71
AAT TGA TAC GAT TGC GCA CAT GGC TAT CTG GGA TC
asn) OPA (tyr asp cys ala his gly tyr leu gly)

SEQ ID NO: 583

SEQ ID NOS: 580-583

FIGURE 33C

sequence Rv1044 predicted by Cole et al. (Nature 393:537-544) and containing seq33A

SEQ ID NO: 584
 SEQ ID NO: 585

1/1	31/11
ttg tgt gca aaa ccg tat cta att gat acg	att gcg cac atg gct atc tgg gat cgc ctc
leu cys ala lys pro tyr leu ile asp thr	ile ala his met ala ile trp asp arg leu
61/21	91/31
gtc gag gtt gcc gcc gag caa cat ggc tac	gtc acc act cgc gat gcg cga gac atc ggc
val glu val ala ala glu gln his gly tyr	val thr thr arg asp ala arg asp ile gly
121/41	151/51
gtc gac cct gtg cag ctc cgc ctc cta gcg	ggg cgc gga cgt ctt gag cgt gtc ggc cga
val asp pro val gln leu arg leu leu ala	gly arg gly arg leu glu arg val gly arg
181/61	211/71
ggt gtg tac cgg gtg ccc gtg ctg ccg cgt	ggt gag cac gac gat ctc gca gcc gca gtg
gly val tyr arg val pro val leu pro arg	gly glu his asp asp leu ala ala ala val
241/81	271/91
tcg tgg act ttg ggg cgt ggc gtt atc tcg	cat gag tcg gcc ttg gcg ctt cat gcc ctc
ser trp thr leu gly arg gly val ile ser	his glu ser ala leu ala leu his ala leu
301/101	331/111
gct gac gtg aac ccg tcg cgc atc cat ctc	acc gtc ccg cgc aac aac cat ccg cgt gcg
ala asp val asn pro ser arg ile his leu	thr val pro arg asn asn his pro arg ala
361/121	391/131
gcc ggg ggc gag ctg tac cga gtt cac cgc	cgc gac ctc cag gca gcc cac gtc act tcg
ala gly gly glu leu tyr arg val his arg	arg asp leu gln ala ala his val thr ser
421/141	451/151
gtc gac gga ata ccc gtc acg acg gtt gcg	cgc acc atc aaa gac tgc gtg aag acg ggc
val asp gly ile pro val thr thr val ala	arg thr ile lys asp cys val lys thr gly
481/161	511/171
acg gat cct tat cag ctt ccg gcc gcg atc	gag cga gcc gaa gcc gag ggc acg ctt cgt
thr asp pro tyr gln leu arg ala ala ile	glu arg ala glu ala glu gly thr leu arg
541/181	571/191
cgt ggg tca gca gct gag cta cgc gct gcg	ctc gat gag acc act gcc gga tta cgc gct
arg gly ser ala ala glu leu arg ala ala	leu asp glu thr thr ala gly leu arg ala
601/201	
cgg ccg aag cga gca tcg gcg tga	
arg pro lys arg ala ser ala	OPA

SEQ ID NOS: 584, 585

FIGURE 33D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv1044

1/1 31/11
 taa ttg tgt gca aaa ccg tat cta att gat acg att gcg cac atg gct atc tgg gat cgc
 OCH (leu cys ala lys pro tyr leu ile asp thr ile ala his met ala ile trp asp arg
 61/21 ~~SEQ ID NO: 587~~ 91/31
 ctc gtc gag gtt gcc gcc gag caa cat ggc tac gtc acg act cgc gat gcg cga gac atc
 leu val glu val ala ala glu gln his gly tyr val thr thr arg asp ala arg asp ile
 121/41 151/51
 ggc gtc gac cct gtg cag ctc cgc ctc cta gcg ggg cgc gga cgt ctt gag cgt gtc ggc
 gly val asp pro val gln leu arg leu leu ala gly arg gly arg leu glu arg val gly
 181/61 211/71
 cga ggt gtg tac cgg gtg ccc gtg ctg ccg cgt ggt gag cac gac gat ctc gca gcc gca
 arg gly val tyr arg val pro val leu pro arg gly glu his asp asp leu ala ala ala
 241/81 271/91
 gtg tcg tgg act ttg ggg cgt ggc gtt atc tcg cat gag tcg gcc ttg gcg ctt cat gcc
 val ser trp thr leu gly arg gly val ile ser his glu ser ala leu ala leu his ala
 301/101 331/111
 ctc gct gac gtg aac ccg tcg cgc atc cat ctc acc gtc ccg cgc aac aac cat ccg cgt
 leu ala asp val asn pro ser arg ile his leu thr val pro arg asn asn his pro arg
 361/121 391/131
 gcg gcc ggg ggc gag ctg tac cga gtt cac cgc cgc gac ctc cag gca gcc cac gtc act
 ala ala gly gly glu leu tyr arg val his arg arg asp leu gln ala ala his val thr
 421/141 451/151
 tcg gtc gac gga ata ccc gtc acg acg gtt gcg cgc acc atc aaa gac tgc gtg aag acg
 ser val asp gly ile pro val thr thr val ala arg thr ile lys asp cys val lys thr
 481/161 511/171
 ggc acg gat cct tat cag ctt cgg gcc gcg atc gag cga gcc gaa gcc gag ggc acg ctt
 gly thr asp pro tyr gln leu arg ala ala ile glu arg ala glu ala glu gly thr leu
 541/181 571/191
 cgt cgt ggg tca gca gct gag cta cgc gct gcg ctc gat gag acc act gcc gga tta cgc
 arg arg gly ser ala ala glu leu arg ala ala leu asp glu thr thr ala gly leu arg
 601/201
 gct cgg ccg aag cga gca tcg gcg tga
 ala arg pro lys arg ala ser ala) OPA

SEQ ID NOS: 586-587

FIGURE 33E

1/1 31/11
 ATC CAA CCT GCT GGG CCT GCG CCT TCG AAT CGA CGG CCA GGC CAC CGC TCG CTG CCG GCA
 ile gln pro ala gly pro ala pro ser asn arg arg pro gly his arg ser leu pro ala
 61/21 91/31
 ACA ACA CCT GGA ATG GGG ACC TTT TCG GTG TTG CTG GTA ACC GGG ACA ACC GGC ACC ACG
 thr thr pro gly met gly thr phe ser val leu leu val thr gly thr thr gly thr thr
 121/41 151/51
 CCT CGG TCG AGA CGT ATC GCG GCA GCG TTG GCC CTG TCG TTG CTG ACA ATT ACC GCT GGC
 pro arg ser arg arg ile ala ala ala leu ala leu ser leu leu thr ile thr ala gly
 181/61 211/71
 CGC CGC ATA TTT GCC GCG CTG CCG CGG GCC GGA TC
 arg arg ile phe ala ala leu pro arg ala gly)

SEQ ID NOS: 588, 589

FIGURE 34A

105/185

SEQ ID NO: 590
 1/1
 61/21
 121/41
 181/61

31/11
 TCC AAC CTG CTG GGC CTG CGC CTT CGA ATC GAC GGC CAG GCC ACC GCT CGC TGC CGG CAA
 (ser asn leu leu gly leu arg leu arg ile asp gly gln ala thr ala arg cys arg gln
 CAA CAC CTG GAA TGG GGA CCT TTT CGG TGT TGC TGG TAA CCG GGA CAA CCG GCA CCA CGC
 gln his leu glu trp gly pro phe arg cys cys trp) OCH (pro gly gln pro ala pro arg
 CTC GGT CGA GAC GTA TCG CGG CAG CGT TGG CCC TGT CGT TGC TGA CAA TTA CCG CTG GCC
 leu gly arg asp val ser arg gln arg trp pro cys arg cys) OPA (gln leu pro leu ala
 GCC GCA TAT TTG CCG CGC TGC CGC GGG CCG GAT C
 ala ala tyr leu pro arg cys arg gly pro asp)

SEQ ID NO: 592

SEQ ID NO: 593

SEQ ID NOS: 590-593

FIGURE 34B

SEQ ID NO: 594
 1/1
 61/21
 121/41
 181/61

31/11
 GAT CCA ACC TGC TGG GCC TGC GCC TTC GAA TCG ACG GCC AGG CCA CCG CTC GCT GCC GGC
 (asp pro thr cys trp ala cys ala phe glu ser thr ala arg pro pro leu ala ala gly
 AAC AAC ACC TGG AAT GGG GAC CTT TTC GGT GTT GCT GGT AAC CGG GAC AAC CGG CAC CAC
 asn asn thr trp asn gly asp leu phe gly val ala gly asn arg asp asn arg his his
 GCC TCG GTC GAG ACG TAT CGC GGC AGC GTT GGC CCT GTC GTT GCT GAC AAT TAC CGC TGG
 ala ser val glu thr tyr arg gly ser val gly pro val val ala asp asn tyr arg trp
 CCG CCG CAT ATT TGC CGC GCT GCC GCG GGC CGG ATC
 pro pro his ile cys arg ala ala ala gly arg ile)

SEQ ID NOS: 594, 595

FIGURE 34C

106/185

ORF according to Cole et al. (Nature 393:537-544) containing seq34A

1/1 31/11
 tag ccg cag ggc cct gcg gct agg cgc ggc cgg tgc cgt tgg ccg cgg cgg caa tcg atg
 AMB pro gln gly pro ala ala arg arg gly arg cys arg trp pro arg arg gln ser met
 61/21 SEQ ID NO: 597 91/31
 ttg cag cag tta caa cgc caa atg gag tct gag cgc atc gtc gag ttc gat cag ctc ggc
 leu gln gln leu gln arg gln met glu ser glu arg ile val glu phe asp gln leu gly
 121/41 151/51
 agg gga gac gtt gcg cag cga cgg atc caa cct gct ggg cct gcg cct tcg aat cga cgg
 arg gly asp val ala gln arg arg ile gln pro ala gly pro ala pro ser asn arg arg
 181/61 211/71
 cca ggc cac cgc tcg ctg ccg gca aca aca cct gga atg ggg acc ttt tcg gtg ttg ctg
 pro gly his arg ser leu pro ala thr thr pro gly met gly thr phe ser val leu leu
 241/81 271/91
 gta acc ggg aca acc ggc acc acg cct cgg tcg aga cgt atc gcg gca gcg ttg gcc ctg
 val thr gly thr thr gly thr thr pro arg ser arg arg ile ala ala ala leu ala leu
 301/101 331/111
 tcg ttg ctg aca att acc gct ggc cgc cgc ata ttt gcc gcg ctg ccg cgg gcc gga tcc
 ser leu leu thr ile thr ala gly arg arg ile phe ala ala leu pro arg ala gly ser
 361/121 391/131
 agg tcg acc tgc cag atc tca ccg cgc agc atc tac gcc gtt cgc tgc aaa ccg ccg act
 arg ser thr cys gln ile ser pro arg ser ile tyr ala val arg cys lys pro pro thr
 421/141 451/151
 gcg acg gca ggc cca ctc tct tgg cat gcg tcc aat gct gcg acg tcc tcg gta gac aag
 ala thr ala gly pro leu ser trp his ala ser asn ala ala thr ser ser val asp lys
 481/161 511/171
 ctc acg ctt ggc ttc atg ccg cag tcc tac cca tgt agt aac aga tag
 leu thr leu gly phe met pro gln ser tyr pro cys ser asn arg)AMB

SEQ ID NOS: 596, 597

FIGURE 34E

1/1 31/11
 CAG TCT GTC GGC AAG GAG GGA CGC ATG CCA CTC TCC GAT CAT GAG CAG CGG ATG CTT GAC
 gln ser val gly lys glu gly arg met pro leu ser asp his glu gln arg met leu asp
 61/21 91/31
 CAG ATC GAG AGC GCT CTC TAC GCC GAA GAT CCC AAG TTC GCA TCG AGT GTC CGT GGC GGG
 gln ile glu ser ala leu tyr ala glu asp pro lys phe ala ser ser val arg gly gly
 121/41 151/51
 GGC TTC CGC GCA CCG ACC GCG CGG CGG CGC CTG CAG GGC GCG GCG TTG TTC ATC ATC GGT
 gly phe arg ala pro thr ala arg arg arg leu gln gly ala ala leu phe ile ile gly
 181/61 211/71
 CTG GGG ATG TTG GTT TCC GGC GTG GCG TTC AAA GAG ACC ATG ATC GGA AGT TTC CCG ATA
 leu gly met leu val ser gly val ala phe lys glu thr met ile gly ser phe pro ile
 241/81 271/91
 CTC AGC GTT TTC GGT TTT GTC GTG ATG TTC GGT GGT GTG GTG TAT GCC ATC ACC GGT CCT
 leu ser val phe gly phe val val met phe gly gly val val tyr ala ile thr gly pro
 301/101 331/111
 CGG TTG TCC GGC AGG ATG GAT CGT GGC GGA TCG GCT GCT GGG GCT TCG CGC CAG CGT CGT
 arg leu ser gly arg met asp arg gly gly ser ala ala gly ala ser arg gln arg arg
 361/121 391/131
 ACC AAG GGG GCC GGG GGC TCA TTC ACC AGC CGT ATG GAA GAT C
 thr lys gly ala gly gly ser phe thr ser arg met glu asp)

SEQ ID NOS: 598, 599

FIGURE 35A

107/185

SEQ ID NO: 600

1/1 31/11
 GAC AGT CTG TCG GCA AGG AGG GAC GCA TGC CAC TCT CCG ATC ATG AGC AGC GGA TGC TTG
 (asp ser leu ser ala arg arg asp ala cys his ser pro ile met ser ser gly cys leu
 61/21 91/31
 ACC AGA TCG AGA GCG CTC TCT ACG CCG AAG ATC CCA AGT TCG CAT CGA GTG TCC GTG GCG
 thr arg ser arg ala leu ser thr pro lys ile pro ser ser his arg val ser val ala
 121/41 151/51
 GGG GCT TCC GCG CAC CGA CCG CGC GGC GGC GCC TGC AGG GCG CGG CGT TGT TCA TCA TCG
 gly ala ser ala his arg pro arg gly gly ala cys arg ala arg arg cys ser ser ser
 181/61 211/71
 GTC TGG GGA TGT TGG TTT CCG GCG TGG CGT TCA AAG AGA CCA TGA TCG GAA GTT TCC CGA
 val trp gly cys trp phe pro ala trp arg ser lys arg pro) OPA (ser glu val ser arg
 241/81 271/91
 TAC TCA GCG TTT TCG GTT TTG TCG TGA TGT TCG GTG GTG TGG TGT ATG CCA TCA CCG GTC
 tyr ser ala phe ser val leu ser) OPA (cys ser val val trp cys met pro ser pro val
 301/101 331/111
 CTC GGT TGT CCG GCA GGA TGG ATC GTG GCG GAT CGG CTG CTG GGG CTT CGC GCC AGC GTC
 leu gly cys pro ala gly trp ile val ala asp arg leu leu gly leu arg ala ser val
 361/121 391/131
 GTA CCA AGG GGG CCG GGG GCT CAT TCA CCA GCC GTA TGG AAG ATC
 val pro arg gly pro gly ala his ser pro ala val trp lys ile)

SEQ ID NO: 602

SEQ ID NO: 603

SEQ ID NOS: 600-603

FIGURE 35B

SEQ ID NO: 604

1/1 31/11
 ACA GTC TGT CGG CAA GGA GGG ACG CAT GCC ACT CTC CGA TCA TGA GCA GCG GAT GCT TGA
 (thr val cys arg gln gly gly thr his ala thr leu arg ser) OPA (ala ala asp ala) OPA
 61/21 91/31
 CCA GAT CGA GAG CGC TCT CTA CGC CGA AGA TCC CAA GTT CGC ATC GAG TGT CCG TGG CGG
 pro asp arg glu arg ser leu arg arg arg ser gln val arg ile glu cys pro trp arg
 121/41 151/51
 GGG CTT CCG CGC ACC GAC CGC GCG GCG GCG CCT GCA GGG CGC GGC GTT GTT CAT CAT CGG
 gly leu pro arg thr asp arg ala ala ala pro ala gly arg gly val val his his arg
 181/61 211/71
 TCT GGG GAT GTT GGT TTC CGG CGT GGC GTT CAA AGA GAC CAT GAT CGG AAG TTT CCC GAT
 ser gly asp val gly phe arg arg gly val gln arg asp his asp arg lys phe pro asp
 241/81 271/91
 ACT CAG CGT TTT CGG TTT TGT CGT GAT GTT CGG TGG TGT GGT GTA TGC CAT CAC CGG TCC
 thr gln arg phe arg phe cys arg asp val arg trp cys gly val cys his his arg ser
 301/101 331/111
 TCG GTT GTC CGG CAG GAT GGA TCG TGG CGG ATC GGC TGC TGG GGC TTC GCG CCA GCG TCG
 ser val val arg gln asp gly ser trp arg ile gly cys trp gly phe ala pro ala ser
 361/121 391/131
 TAC CAA GGG GGC CGG GGG CTC ATT CAC CAG CCG TAT GGA AGA TC
 tyr gln gly gly arg gly leu ile his gln pro tyr gly arg)

SEQ ID NO: 606

SEQ ID NOS: 604-607

FIGURE 35C

108/185

sequence Rv2169c predicted by Cole et al. (Nature 393:537-544) and partially containing seq35A

1/1 31/11
 atg cca ctc tcc gat cat gag cag cgg atg ctt gac cag atc gag agc gct ctc tac gcc
 (Met pro leu ser asp his glu gln arg met leu asp gln ile glu ser ala leu tyr ala
 61/21 91/31
 gaa gat ccc aag ttc gca tcg agt gtc cgt ggc ggg ggc ttc cgc gca ccg acc gcg cgg
 glu asp pro lys phe ala ser ser val arg gly gly gly phe arg ala pro thr ala arg
 121/41 151/51
 cgg cgc ctg cag ggc gcg gcg ttg ttc atc atc ggt ctg ggg atg ttg gtt tcc ggc gtg
 arg arg leu gln gly ala ala leu phe ile ile gly leu gly met leu val ser gly val
 181/61 211/71
 gcg ttc aaa gag acc atg atc gga agt ttc ccg ata ctc agc gtt ttc ggt ttt gtc gtg
 ala phe lys glu thr met ile gly ser phe pro ile leu ser val phe gly phe val val
 241/81 271/91
 atg ttc ggt ggt gtg gtg tat gcc atc acc ggt cct cgg ttg tcc ggc agg atg gat cgt
 met phe gly gly val val tyr ala ile thr gly pro arg leu ser gly arg met asp arg
 301/101 331/111
 ggc gga tcg gct gct ggg gct tcg cgc cag cgt cgt acc aag ggg gcc ggg ggc tca ttc
 gly gly ser ala ala gly ala ser arg gln arg arg thr lys gly ala gly gly ser phe
 361/121 391/131
 acc agc cgt atg gaa gat cgg ttc cgg cgc cgc ttc gac gag taa
 thr ser arg met glu asp arg phe arg arg arg phe asp glu) OCH

SEQ ID NOS: 608-609

FIGURE 35D

ORF according to Cole et al. (Nature 393:537-544) and containing Rv2169c

1/1 31/11
 tga cag tct gtc ggc aag gag gga cgc atg cca ctc tcc gat cat gag cag cgg atg ctt
 OPA (gln ser val gly lys glu gly arg met pro leu ser asp his glu gln arg met leu
 61/21 91/31
 gac cag atc gag agc gct ctc tac gcc gaa gat ccc aag ttc gca tcg agt gtc cgt ggc
 asp gln ile glu ser ala leu tyr ala glu asp pro lys phe ala ser ser val arg gly
 121/41 151/51
 ggg ggc ttc cgc gca ccg acc gcg cgg cgg cgc ctg cag ggc gcg gcg ttg ttc atc atc
 gly gly phe arg ala pro thr ala arg arg arg leu gln gly ala ala leu phe ile ile
 181/61 211/71
 ggt ctg ggg atg ttg gtt tcc ggc gtg gcg ttc aaa gag acc atg atc gga agt ttc ccg
 gly leu gly met leu val ser gly val ala phe lys glu thr met ile gly ser phe pro
 241/81 271/91
 ata ctc agc gtt ttc ggt ttt gtc gtg atg ttc ggt ggt gtg gtg tat gcc atc acc ggt
 ile leu ser val phe gly phe val val met phe gly gly val val tyr ala ile thr gly
 301/101 331/111
 cct cgg ttg tcc ggc agg atg gat cgt ggc gga tcg gct gct ggg gct tcg cgc cag cgt
 pro arg leu ser gly arg met asp arg gly gly ser ala ala gly ala ser arg gln arg
 361/121 391/131
 cgt acc aag ggg gcc ggg ggc tca ttc acc agc cgt atg gaa gat cgg ttc cgg cgc cgc
 arg thr lys gly ala gly gly ser phe thr ser arg met glu asp arg phe arg arg arg
 421/141
 ttc gac gag taa
 phe asp glu) OCH

SEQ ID NOS: 610, 611

FIGURE 35E

109/185

SEQ ID NO: 612

SEQ ID NO: 613

1/1 31/11
 GAC CTG GGA CGA AGA CGA CGG CAG CAG CCG CAA TCA GAT CTA CCC GGT CCT GGT CAA CGT
 (asp leu gly arg arg arg arg gln gln pro gln ser asp leu pro gly pro gly gln arg
 61/21 91/31
 CAA TGG ACA CCC GAC TAC GGT GCG CCT GCG CGG CTC GAC AAT GCG CGG TTC CTG TTG CCC
 gln trp thr pro asp tyr gly ala pro ala arg leu asp asn ala arg phe leu leu pro
 121/41 151/51
 GTG GTC GGA GTG CCA CCC GAC CAG GCC ACC GAC TTC GGC TCC GCT GTT GCA CCA GAA ACG
 val val gly val pro pro asp gln ala thr asp phe gly ser ala val ala pro glu thr
 181/61 211/71
 ACG GCG CCG GTC TGG ATC ACC ATG CTG TGG CCG CTG GCC GAC CGG CCC CGG TTG GCC CCC
 thr ala pro val trp ile thr met leu trp pro leu ala asp arg pro arg leu ala pro
 241/81 271/91
 GGG GCA CCC GGT GGC ACC GTT CCC GTC CGG CTG GTC GAC GAC GAC CTG GCA AAC TCG CTG
 gly ala pro gly gly thr val pro val arg leu val asp asp asp leu ala asn ser leu
 301/101 331/111
 GCC AAC GGC GGC CGG CTG GAC ATC CTC CTG TCG GCG GCC GAG TTC GCC ACC AAC CGG GAA
 ala asn gly gly arg leu asp ile leu leu ser ala ala glu phe ala thr asn arg glu
 361/121 391/131
 GTC GAC CCC GAC GGC GCC GTC GGC CGA GCG CTG TGC CTG GCC ATC GAC CCA GAT C
 val asp pro asp gly ala val gly arg ala leu cys leu ala ile asp pro asp)

SEQ ID NOS: 612-613

FIGURE 36A

SEQ ID NO: 614

SEQ ID NO: 615

1/1 31/11
 ACC TGG GAC GAA GAC GAC GGC AGC AGC CGC AAT CAG ATC TAC CCG GTC CTG GTC AAC GTC
 (thr trp asp glu asp asp gly ser ser arg asn gln ile tyr pro val leu val asn val
 61/21 91/31
 AAT GGA CAC CCG ACT ACG GTG CGC CTG CGC GGC TCG ACA ATG CGC GGT TCC TGT TGC CCG
 asn gly his pro thr thr val arg leu arg gly ser thr met arg gly ser cys cys pro
 121/41 151/51
 TGG TCG GAG TGC CAC CCG ACC AGG CCA CCG ACT TCG GCT CCG CTG TTG CAC CAG AAA CGA
 trp ser glu cys his pro thr arg pro pro thr ser ala pro leu leu his gln lys arg
 181/61 211/71
 CGG CGC CGG TCT GGA TCA CCA TGC TGT GGC CGC TGG CCG ACC GGC CCC GGT TGG CCC CCG
 arg arg arg ser gly ser pro cys cys gly arg trp pro thr gly pro gly trp pro pro
 241/81 271/91
 GGG CAC CCG GTG GCA CCG TTC CCG TCC GGC TGG TCG ACG ACG ACC TGG CAA ACT CGC TGG
 gly his pro val ala pro phe pro ser gly trp ser thr thr thr trp gln thr arg trp
 301/101 331/111
 CCA ACG GCG GCC GGC TGG ACA TCC TCC TGT CGG CGG CCG AGT TCG CCA CCA ACC GGG AAG
 pro thr ala ala gly trp thr ser ser cys arg arg pro ser ser pro pro thr gly lys
 361/121 391/131
 TCG ACC CCG ACG GCG CCG TCG GCC GAG CGC TGT GCC TGG CCA TCG ACC CAG ATC
 ser thr pro thr ala pro ser ala glu arg cys ala trp pro ser thr gln ile)

SEQ ID NOS: 614-615

FIGURE 36B

110/185

SEQ ID NO: 616

SEQ ID NO: 617

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1/1                               31/11
CCT GGG ACG AAG ACG ACG GCA GCA GCC GCA ATC AGA TCT ACC CGG TCC TGG TCA ACG TCA
(pro gly thr lys thr thr ala ala ala ala ile arg ser thr arg ser trp ser thr ser
61/21                               91/31
ATG GAC ACC CGA CTA CGG TGC GCC TGC GCG GCT CGA CAA TGC GCG GTT CCT GTT GCC CGT
met asp thr arg leu arg cys ala cys ala ala arg gln cys ala val pro val ala arg
121/41                               151/51
GGT CGG AGT GCC ACC CGA CCA GGC CAC CGA CTT CGG CTC CGC TGT TGC ACC AGA AAC GAC
gly arg ser ala thr arg pro gly his arg leu arg leu arg cys cys thr arg asn asp
181/61                               211/71
GGC GCC GGT CTG GAT CAC CAT GCT GTG GCC GCT GGC CGA CCG GCC CCG GTT GGC CCC CGG
gly ala gly leu asp his his ala val ala ala gly arg pro ala pro val gly pro arg
241/81                               271/91
GGC ACC CGG TGG CAC CGT TCC CGT CCG GCT GGT CGA CGA CGA CCT GGC AAA CTC GCT GGC
gly thr arg trp his arg ser arg pro ala gly arg arg arg pro gly lys leu ala gly
301/101                               331/111
CAA CGG CGG CCG GCT GGA CAT CCT CCT GTC GGC GGC CGA GTT CGC CAC CAA CCG GGA AGT
gln arg arg pro ala gly his pro pro val gly gly arg val arg his gln pro gly ser
361/121                               391/131
CGA CCC CGA CGG CGC CGT CGG CCG AGC GCT GTG CCT GGC CAT CGA CCC AGA TC
arg pro arg arg arg arg arg pro ser ala val pro gly his arg pro arg)

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SEQ ID NOS: 616, 617

FIGURE 36C

SEQ ID NO: 618

SEQ ID NO: 619

Coding sequence Rv3909 predicted by Cole et al., 1998 (Nature 393 537-544) containing Seq 36A

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1/1                               31/11
GTG ACC GCA CTG CAA CTC GGC TGG GCC GCT TTG GCG CGC GTC ACC TCA GCG ATC GGC GTC
(met thr ala leu gln leu gly trp ala ala leu ala arg val thr ser ala ile gly val
61/21                               91/31
GTG GCC GGC CTC GGG ATG GCG CTC ACG GTA CCG TCG GCG GCA CCG CAC GCG CTC GCA GGC
val ala gly leu gly met ala leu thr val pro ser ala ala pro his ala leu ala gly
121/41                               151/51
GAG CCC AGC CCG ACG CCT TTT GTC CAG GTC CGC ATC GAT CAG GTG ACC CCG GAC GTG GTG
glu pro ser pro thr pro phe val gln val arg ile asp gln val thr pro asp val val
181/61                               211/71
ACC ACT TCC AGC GAA CCC CAT GTC ACC GTC AGC GGA ACG GTG ACC AAT ACC GGT GAC CGC
thr thr ser ser glu pro his val thr val ser gly thr val thr asn thr gly asp arg
241/81                               271/91
CCA GTC CGC GAT GTG ATG GTC CGG CTT GAG CAC GCC GCC GCG GTC ACG TCG TCA ACG GCG
pro val arg asp val met val arg leu glu his ala ala ala val thr ser ser thr ala
301/101                               331/111
TTA CGC ACC TCG CTC GAC GGC GGC ACC GAC CAG TAC CAG CCG GCC GCG GAC TTC CTC ACG
leu arg thr ser leu asp gly gly thr asp gln tyr gln pro ala ala asp phe leu thr

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SEQ ID NOS: 618-619

FIGURE 36D

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361/121                                391/131
GTC GCC CCC GAA CTA GAC CGC GGG CAA GAG GCC GGC TTT ACC CTC TCG GCC CCG CTG CGC
val ala pro glu leu asp arg gly gln glu ala gly phe thr leu ser ala pro leu arg
421/141                                451/151
TCG CTG ACC AGG CCG TCG TTG GCC GTC AAC CAG CCC GGG ATC TAC CCG GTC CTG GTC AAC
ser leu thr arg pro ser leu ala val asn gln pro gly ile tyr pro val leu val asn
481/161                                511/171
GTC AAT GGG ACA CCC GAC TAC GGT GCG CCT GCG CGG CTC GAC AAT GCG CGG TTC CTG TTG
val asn gly thr pro asp tyr gly ala pro ala arg leu asp asn ala arg phe leu leu
541/181                                571/191
CCC GTG GTC GGA GTG CCA CCC GAC CAG GCC ACC GAC TTC GGC TCC GCT GTT GCA CCA GAA
pro val val gly val pro pro asp gln ala thr asp phe gly ser ala val ala pro glu
601/201                                631/211
ACG ACG GCG CCG GTC TGG ATC ACC ATG CTG TGG CCG CTG GCC GAC CGG CCC CGG TTG GCC
thr thr ala pro val trp ile thr met leu trp pro leu ala asp arg pro arg leu ala
661/221                                691/231
CCC GGG GCA CCC GGT GGC ACC GTT CCC GTC CGG CTG GTC GAC GAC GAC CTG GCA AAC TCG
pro gly ala pro gly gly thr val pro val arg leu val asp asp asp leu ala asn ser
721/241                                751/251
CTG GCC AAC GGC GGC CGG CTG GAC ATC CTC CTG TCG GCG GCC GAG TTC GCC ACC AAC CGG
leu ala asn gly gly arg leu asp ile leu leu ser ala ala glu phe ala thr asn arg
781/261                                811/271
GAA GTC GAC CCC GAC GGC GCC GTC GGC CGA GCG CTG TGC CTG GCC ATC GAC CCA GAT CTA
glu val asp pro asp gly ala val gly arg ala leu cys leu ala ile asp pro asp leu
841/281                                871/291
CTC ATC ACC GTC AAT GCG ATG ACC GGC GGC TAC GTC GTG TCC GAC TCG CCC GAC GGG GCC
leu ile thr val asn ala met thr gly gly tyr val val ser asp ser pro asp gly ala
901/301                                931/311
GCT CAA CTA CCG GGC ACC CCG ACC CAC CCG GGC ACC GGC CAG GCC GCC GCA TCC AGC TGG
ala gln leu pro gly thr pro thr his pro gly thr gly gln ala ala ala ser ser trp
961/321                                991/331
CTG GAT CGA TTG CGG ACG CTA GTC CAC CGG ACA TGC GTG ACG CCG CTG CCT TTT GCC CAA
leu asp arg leu arg thr leu val his arg thr cys val thr pro leu pro phe ala gln
1021/341                                1051/351
GCC GAC CTG GAT GCT TTG CAG CGG GTT AAT GAT CCG AGG CTG AGC GCG ATC GCA ACC ATC
ala asp leu asp ala leu gln arg val asn asp pro arg leu ser ala ile ala thr ile
1081/361                                1111/371
AGC CCC GCC GAC ATC GTC GAC CGC ATC CTG GAT GTC AGC TCC ACC CGC GGC GCA ACC GTG
ser pro ala asp ile val asp arg ile leu asp val ser ser thr arg gly ala thr val
1141/381                                1171/391
CTG CCC GAC GGC CCG TTG ACC GGC CGG GCG ATC AAC TTG CTC AGC ACC CAC GGC AAC ACG
leu pro asp gly pro leu thr gly arg ala ile asn leu leu ser thr his gly asn thr
1201/401                                1231/411
GTT GCC GTC GCG GCC GCC GAT TTT AGC CCC GAG GAA CAG CAG GGT TCG TCC CAG ATC GGC
val ala val ala ala ala asp phe ser pro glu glu gln gln gly ser ser gln ile gly
1261/421                                1291/431
TCC GCG CTC TTA CCC GCT ACC GCG CCC CGG CGG TTG TCC CCG CGG GTG GTA GCG GCG CCG
ser ala leu leu pro ala thr ala pro arg arg leu ser pro arg val val ala ala pro
1321/441                                1351/451
TTT GAT CCC GCG GTC GGG GCC GCG CTG GCC GCC GCG GGA ACA AAC CCG ACC GTT CCT ACC
phe asp pro ala val gly ala ala leu ala ala ala gly thr asn pro thr val pro thr
1381/461                                1411/471
TAT CTA GAT CCC TCG TTG TTC GTT CGG ATC GCG CAT GAA TCG ATC ACC GCG CGC CGC CAG
tyr leu asp pro ser leu phe val arg ile ala his glu ser ile thr ala arg arg gln

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SEQ ID NDS: 618-619

FIGURE 36D (continued 1)

1441/481	1471/491
GAC GCC TTG GGC GCA ATG CTG TGG CGC AGC	TTG GAG CCG AAT GCC GCG CCC CGT ACC CAA
asp ala leu gly ala met leu trp arg ser	leu glu pro asn ala ala pro arg thr gln
1501/501	1531/511
ATC CTG GTG CCG CCG GCG TCG TGG AGC CTG	GCC AGC GAC GAC GCG CAG GTC ATC CTG ACC
ile leu val pro pro ala ser trp ser leu	ala ser asp asp ala gln val ile leu thr
1561/521	1591/531
GCG CTG GCC ACC GCC ATC CGG TCT GGC CTG	GCC GTG CCG CGA CCA CTA CCG GCG GTG ATC
ala leu ala thr ala ile arg ser gly leu	ala val pro arg pro leu pro ala val ile
1621/541	1651/551
GCT GAC GCC GCG GCC CGC ACC GAG CCA CCG	GAA CCC CCG GGC GCT TAC AGC GCC GCT CGC
ala asp ala ala ala arg thr glu pro pro	glu pro pro gly ala tyr ser ala ala arg
1681/561	1711/571
GGC CGG TTC AAT GAC GAC ATC ACC ACG CAG	ATC GGC GGG CAG GTT GCC CGG CTA TGG AAG
gly arg phe asn asp asp ile thr thr gln	ile gly gly gln val ala arg leu trp lys
1741/581	1771/591
CTG ACC TCG GCG TTG ACC ATC GAT GAC CGC	ACC GGG CTG ACC GGC GTG CAG TAC ACC GCA
leu thr ser ala leu thr ile asp asp arg	thr gly leu thr gly val gln tyr thr ala
1801/601	1831/611
CCA CTA CGC GAG GAC ATG TTG CGC GCG CTG	AGC CAA TCG CTA CCA CCC GAT ACC CGC AAC
pro leu arg glu asp met leu arg ala leu	ser gln ser leu pro pro asp thr arg asn
1861/621	1891/631
GGG CTG GCC CAG CAG CGG CTG GCC GTC GTT	GGA AAG ACG ATC GAC GAT CTT TTC GGC GCG
gly leu ala gln gln arg leu ala val val	gly lys thr ile asp asp leu phe gly ala
1921/641	1951/651
GTG ACC ATC GTC AAC CCG GGC GGC TCC TAC	ACT CTG GCC ACC GAG CAC AGT CCG CTG CCG
val thr ile val asn pro gly gly ser tyr	thr leu ala thr glu his ser pro leu pro
1981/661	2011/671
TTG GCG CTG CAT AAT GGC CTC GCC GTG CCA	ATC CGG GTC CGG CTA CAG GTC GAT GCT CCG
leu ala leu his asn gly leu ala val pro	ile arg val arg leu gln val asp ala pro
2041/681	2071/691
CCC GGG ATG ACG GTG GCC GAT GTC GGT CAG	ATC GAG CTA CCG CCC GGG TAC CTG CCG CTA
pro gly met thr val ala asp val gly gln	ile glu leu pro pro gly tyr leu pro leu
2101/701	2131/711
CGA GTA CCA ATC GAG GTG AAC TTC ACA CAG	CGG GTT GCC GTC GAC GTG TCG CTG CCG ACC
arg val pro ile glu val asn phe thr gln	arg val ala val asp val ser leu arg thr
2161/721	2191/731
CCC GAC GGC GTC GCG CTG GGT GAA CCG GTG	CGG TTG TCG GTG CAC TCC AAC GCC TAC GGC
pro asp gly val ala leu gly glu pro val	arg leu ser val his ser asn ala tyr gly
2221/741	2251/751
AAG GTG TTG TTC GCG ATC ACG CTA TCC GCT	GCG GCC GTG CTG GTA ACG CTG GCG GGC CGG
lys val leu phe ala ile thr leu ser ala	ala ala val leu val thr leu ala gly arg
2281/761	2311/771
CGC CTT TGG CAC CGG TTC CGT GGC CAG CCT	GAT CGC GCC GAC CTG GAT CGC CCC GAC CTG
arg leu trp his arg phe arg gly gln pro	asp arg ala asp leu asp arg pro asp leu
2341/781	2371/791
CCT ACC GGC AAA CAC GCC CCG CAG CGC CGT	GCC GTA GCC AGT CGG GAT GAC GAA AAG CAC
pro thr gly lys his ala pro gln arg arg	ala val ala ser arg asp asp glu lys his
2401/801	
CGG GTA TGA	
arg val) OPA	

SEQ ID NOS: 618-619

FIGURE 36D (continued 2)

ORF according to Cole et al., 1998 (Nature 393 537-544) and containing Rv 3909.

1/1 31/11
 TGA CTC AGC ACC GGG TCA GCA CAA CGG TCC CGG GCC GGG GCC GTG ACC GCA CTG CAA CTC
 OPA (leu ser thr gly ser ala gln arg ser arg ala gly ala val thr ala leu gln leu
 61/21 *SEQ ID NO: 621* 91/31
 GGC TGG GCC GCT TTG GCG CGC GTC ACC TCA GCG ATC GGC GTC GTG GCC GGC CTC GGG ATG
 gly trp ala ala leu ala arg val thr ser ala ile gly val val ala gly leu gly met
 121/41 151/51
 GCG CTC ACG GTA CCG TCG GCG GCA CCG CAC GCG CTC GCA GGC GAG CCC AGC CCG ACG CCT
 ala leu thr val pro ser ala ala pro his ala leu ala gly glu pro ser pro thr pro
 181/61 211/71
 TTT GTC CAG GTC CGC ATC GAT CAG GTG ACC CCG GAC GTG GTG ACC ACT TCC AGC GAA CCC
 phe val gln val arg ile asp gln val thr pro asp val val thr thr ser ser glu pro
 241/81 271/91
 CAT GTC ACC GTC AGC GGA ACG GTG ACC AAT ACC GGT GAC CGC CCA GTC CGC GAT GTG ATG
 his val thr val ser gly thr val thr asn thr gly asp arg pro val arg asp val met
 301/101 331/111
 GTC CGG CTT GAG CAC GCC GCC GCG GTC ACG TCG TCA ACG GCG TTA CGC ACC TCG CTC GAC
 val arg leu glu his ala ala ala val thr ser ser thr ala leu arg thr ser leu asp
 361/121 391/131
 GGC GGC ACC GAC CAG TAC CAG CCG GCC GCG GAC TTC CTC ACG GTC GCC CCC GAA CTA GAC
 gly gly thr asp gln tyr gln pro ala ala asp phe leu thr val ala pro glu leu asp
 421/141 451/151
 CGC GGG CAA GAG GCC GGC TTT ACC CTC TCG GCC CCG CTG CGC TCG CTG ACC AGG CCG TCG
 arg gly gln glu ala gly phe thr leu ser ala pro leu arg ser leu thr arg pro ser
 481/161 511/171
 TTG GCC GTC AAC CAG CCC GGG ATC TAC CCG GTC CTG GTC AAC GTC AAT GGG ACA CCC GAC
 leu ala val asn gln pro gly ile tyr pro val leu val asn val asn gly thr pro asp
 541/181 571/191
 TAC GGT GCG CCT GCG CGG CTC GAC AAT GCG CGG TTC CTG TTG CCC GTG GTC GGA GTG CCA
 tyr gly ala pro ala arg leu asp asn ala arg phe leu leu pro val val gly val pro
 601/201 631/211
 CCC GAC CAG GCC ACC GAC TTC GGC TCC GCT GTT GCA CCA GAA ACG ACG GCG CCG GTC TGG
 pro asp gln ala thr asp phe gly ser ala val ala pro glu thr thr ala pro val trp
 661/221 691/231
 ATC ACC ATG CTG TGG CCG CTG GCC GAC CGG CCC CGG TTG GCC CCC GGG GCA CCC GGT GGC
 ile thr met leu trp pro leu ala asp arg pro arg leu ala pro gly ala pro gly gly
 721/241 751/251
 ACC GTT CCC GTC CGG CTG GTC GAC GAC GAC CTG GCA AAC TCG CTG GCC AAC GGC GGC CGG
 thr val pro val arg leu val asp asp asp leu ala asn ser leu ala asn gly gly arg
 781/261 811/271
 CTG GAC ATC CTC CTG TCG GCG GCC GAG TTC GCC ACC AAC CGG GAA GTC GAC CCC GAC GGC
 leu asp ile leu leu ser ala ala glu phe ala thr asn arg glu val asp pro asp gly
 841/281 871/291
 GCC GTC GGC CGA GCG CTG TGC CTG GCC ATC GAC CCA GAT CTA CTC ATC ACC GTC AAT GCG
 ala val gly arg ala leu cys leu ala ile asp pro asp leu leu ile thr val asn ala
 901/301 931/311
 ATG ACC GGC GGC TAC GTC GTG TCC GAC TCG CCC GAC GGG GCC GCT CAA CTA CCG GGC ACC
 met thr gly gly tyr val val ser asp ser pro asp gly ala ala gln leu pro gly thr
 961/321 991/331
 CCG ACC CAC CCG GGC ACC GGC CAG GCC GCC GCA TCC AGC TGG CTG GAT CGA TTG CGG ACG
 pro thr his pro gly thr gly gln ala ala ala ser ser trp leu asp arg leu arg thr

SEQ ID NDS: 620-621

FIGURE 36E

1021/341	1051/351
CTA GTC CAC CGG ACA TGC GTG ACG CCG CTG	CCT TTT GCC CAA GCC GAC CTG GAT GCT TTG
leu val his arg thr cys val thr pro leu	pro phe ala gln ala asp leu asp ala leu
1081/361	1111/371
CAG CGG GTT AAT GAT CCG AGG CTG AGC GCG	ATC GCA ACC ATC AGC CCC GCC GAC ATC GTC
gln arg val asn asp pro arg leu ser ala	ile ala thr ile ser pro ala asp ile val
1141/381	1171/391
GAC CGC ATC CTG GAT GTC AGC TCC ACC CCG	GGC GCA ACC GTG CTG CCC GAC GGC CCG TTG
asp arg ile leu asp val ser ser thr arg	gly ala thr val leu pro asp gly pro leu
1201/401	1231/411
ACC GGC CGG GCG ATC AAC TTG CTC AGC ACC	CAC GGC AAC ACG GTT GCC GTC GCG GCC GCC
thr gly arg ala ile asn leu leu ser thr	his gly asn thr val ala val ala ala ala
1261/421	1291/431
GAT TTT AGC CCC GAG GAA CAG CAG GGT TCG	TCC CAG ATC GGC TCC GCG CTC TTA CCC GCT
asp phe ser pro glu glu gln gln gly ser	ser gln ile gly ser ala leu leu pro ala
1321/441	1351/451
ACC GCG CCC CGG CGG TTG TCC CCG CCG GTG	GTA GCG GCG CCG TTT GAT CCC GCG GTC GGG
thr ala pro arg arg leu ser pro arg val	val ala ala pro phe asp pro ala val gly
1381/461	1411/471
GCC GCG CTG GCC GCC GCG GGA ACA AAC CCG	ACC GTT CCT ACC TAT CTA GAT CCC TCG TTG
ala ala leu ala ala ala gly thr asn pro	thr val pro thr tyr leu asp pro ser leu
1441/481	1471/491
TTC GTT CGG ATC GCG CAT GAA TCG ATC ACC	GCG GCG GCG CAG GAC GCC TTG GGC GCA ATG
phe val arg ile ala his glu ser ile thr	ala arg arg gln asp ala leu gly ala met
1501/501	1531/511
CTG TGG CGC AGC TTG GAG CCG AAT GCC GCG	CCC CGT ACC CAA ATC CTG GTG CCG CCG GCG
leu trp arg ser leu glu pro asn ala ala	pro arg thr gln ile leu val pro pro ala
1561/521	1591/531
TCG TGG AGC CTG GCC AGC GAC GAC GCG CAG	GTC ATC CTG ACC GCG CTG GCC ACC GCC ATC
ser trp ser leu ala ser asp asp ala gln	val ile leu thr ala leu ala thr ala ile
1621/541	1651/551
CGG TCT GGC CTG GCC GTG CCG CGA CCA CTA	CCG GCG GTG ATC GCT GAC GCC GCG GCC CGC
arg ser gly leu ala val pro arg pro leu	pro ala val ile ala asp ala ala ala arg
1681/561	1711/571
ACC GAG CCA CCG GAA CCC CCG GGC GCT TAC	AGC GCC GCT CGC GGC CGG TTC AAT GAC GAC
thr glu pro pro glu pro pro gly ala tyr	ser ala ala arg gly arg phe asn asp asp
1741/581	1771/591
ATC ACC ACG CAG ATC GGC GGG CAG GTT GCC	CGG CTA TGG AAG CTG ACC TCG GCG TTG ACC
ile thr thr gln ile gly gly gln val ala	arg leu trp lys leu thr ser ala leu thr
1801/601	1831/611
ATC GAT GAC CGC ACC GGG CTG ACC GGC GTG	CAG TAC ACC GCA CCA CTA CGC GAG GAC ATG
ile asp asp arg thr gly leu thr gly val	gln tyr thr ala pro leu arg glu asp met
1861/621	1891/631
TTG CGC GCG CTG AGC CAA TCG CTA CCA CCC	GAT ACC CGC AAC GGG CTG GCC CAG CAG CGG
leu arg ala leu ser gln ser leu pro pro	asp thr arg asn gly leu ala gln gln arg
1921/641	1951/651
CTG GCC GTC GTT GGA AAG ACG ATC GAC GAT	CTT TTC GGC GCG GTG ACC ATC GTC AAC CCG
leu ala val val gly lys thr ile asp asp	leu phe gly ala val thr ile val asn pro
1981/661	2011/671
GGC GGC TCC TAC ACT CTG GCC ACC GAG CAC	AGT CCG CTG CCG TTG GCG CTG CAT AAT GGC
gly gly ser tyr thr leu ala thr glu his	ser pro leu pro leu ala leu his asn gly

SEQ ID NOS: 620-621

FIGURE 36E (continued 1)

115/185

2041/681	2071/691
CTC GCC GTG CCA ATC CGG GTC CGG CTA CAG	GTC GAT GCT CCG CCC GGG ATG ACG GTG GCC
leu ala val pro ile arg val arg leu gln	val asp ala pro pro gly met thr val ala
2101/701	2131/711
GAT GTC GGT CAG ATC GAG CTA CCG CCC GGG	TAC CTG CCG CTA CGA GTA CCA ATC GAG GTG
asp val gly gln ile glu leu pro pro gly	tyr leu pro leu arg val pro ile glu val
2161/721	2191/731
AAC TTC ACA CAG CGG GTT GCC GTC GAC GTG	TCG CTG CGG ACC CCC GAC GGC GTC GCG CTG
asn phe thr gln arg val ala val asp val	ser leu arg thr pro asp gly val ala leu
2221/741	2251/751
GGT GAA CCG GTG CGG TTG TCG GTG CAC TCC	AAC GCC TAC GGC AAG GTG TTG TTC GCG ATC
gly glu pro val arg leu ser val his ser	asn ala tyr gly lys val leu phe ala ile
2281/761	2311/771
ACG CTA TCC GCT GCG GCC GTG CTG GTA ACG	CTG GCG GGC CGG CGC CTT TGG CAC CGG TTC
thr leu ser ala ala ala val leu val thr	leu ala gly arg arg leu trp his arg phe
2341/781	2371/791
CGT GGC CAG CCT GAT CGC GCC GAC CTG GAT	CGC CCC GAC CTG CCT ACC GGC AAA CAC GCC
arg gly gln pro asp arg ala asp leu asp	arg pro asp leu pro thr gly lys his ala
2401/801	2431/811
CCG CAG CGC CGT GCC GTA GCC AGT CGG GAT	GAC GAA AAG CAC CGG GTA TGA
pro gln arg arg ala val ala ser arg asp	asp glu lys his arg val) OPA

SEQ ID NOS: 620-621

FIGURE 36E (continued 2)

SEQ ID NO: 622
 1/1
 82a ID NO: 623-1

1/1	31/11
ATC CGC GCG TTG GCG TCG CAT CCG AAC ATC	GTC GGA GTC AAG GAC GCC AAA GCC GAC CTG
(ile arg ala leu ala ser his pro asn ile	val gly val lys asp ala lys ala asp leu
61/21	91/31
CAC AGC GGC GCC CAA ATC ATG GCC GAC ACC	GGA CTG GCC TAC TAT TCC GGC GAC GAC GCG
his ser gly ala gln ile met ala asp thr	gly leu ala tyr tyr ser gly asp asp ala
121/41	151/51
CTC AAC CTG CCC TGG CTG GCC ATG GGC GCC	ACG GGC TTC ATC AGC GTG ATT GCC CAC CTG
leu asn leu pro trp leu ala met gly ala	thr gly phe ile ser val ile ala his leu
181/61	211/71
GCA GCC GGG CAG CTT CGA GAG TTG TTG TCC	GCC TTC GGT TCT GGG GAT ATC GCC ACC GCC
ala ala gly gln leu arg glu leu leu ser	ala phe gly ser gly asp ile ala thr ala
241/81	
CGC AAG ATC	
arg lys ile)	

SEQ ID NOS: 622-623

FIGURE 37A

116/185

SEQ ID NO: 624
SEQ ID NO: 625

1/1 31/11
GAT CCG CGC GTT GGC GTC GCA TCC GAA CAT CGT CGG AGT CAA GGA CGC CAA AGC CGA CCT
(asp pro arg val gly val ala ser glu his arg arg ser gln gly arg gln ser arg pro
61/21 91/31
GCA CAG CGG CGC CCA AAT CAT GGC CGA CAC CGG ACT GGC CTA CTA TTC CGG CGA CGA CGC
ala gln arg arg pro asn his gly arg his arg thr gly leu leu phe arg arg arg arg
121/41 151/51
GCT CAA CCT GCC CTG GCT GGC CAT GGG CGC CAC GGG CTT CAT CAG CGT GAT TGC CCA CCT
ala gln pro ala leu ala gly his gly arg his gly leu his gln arg asp cys pro pro
181/61 211/71
GGC AGC CGG GCA GCT TCG AGA GTT GTT GTC CGC CTT CGG TTC TGG GGA TAT CGC CAC CGC
gly ser arg ala ala ser arg val val val arg leu arg phe trp gly tyr arg his arg
241/81
CCG CAA GAT C
pro gln asp)

SEQ ID NOS: 624-625

FIGURE 37B

SEQ ID NO: 626
SEQ ID NO: 627

1/1 31/11
TCC GCG CGT TGG CGT CGC ATC CGA ACA TCG TCG GAG TCA AGG ACG CCA AAG CCG ACC TGC
(ser ala arg trp arg arg ile arg thr ser ser glu ser arg thr pro lys pro thr cys
61/21 91/31
ACA GCG GCG CCC AAA TCA TGG CCG ACA CCG GAC TGG CCT ACT ATT CCG GCG ACG ACG CGC
thr ala ala pro lys ser trp pro thr pro asp trp pro thr ile pro ala thr thr arg
121/41 151/51
TCA ACC TGC CCT GGC TGG CCA TGG GCG CCA CGG GCT TCA TCA GCG TGA TTG CCC ACC TGG
ser thr cys pro gly trp pro trp ala pro arg ala ser ser ala) OPA (leu pro thr trp
181/61 211/71
CAG CCG GGC AGC TTC GAG AGT TGT TGT CCG CCT TCG GTT CTG GGG ATA TCG CCA CCG CCC
gln pro gly ser phe glu ser cys cys pro pro ser val leu gly ile ser pro pro pro
241/81
GCA AGA TC
ala arg)

SEQ ID NOS: 626-628

FIGURE 37C

117/185

Coding sequence Rv2753c predicted by Cole et al., 1998 (Nature 393 537-544) containing Seq 37A

1/1 31/11
 GTG ACC ACC GTC GGA TTC GAC GTC GCA GCG CGC CTA GGA ACC CTG CTG ACC GCG ATG GTG
 val thr thr val gly phe asp val ala ala arg leu gly thr leu leu thr ala met val
 61/21 91/31
 ACA CCG TTT AGC GGC GAT GGC TCC CTG GAC ACC GCC ACC GCG GCG CGG CTG GCC AAC CAC
 thr pro phe ser gly asp gly ser leu asp thr ala thr ala ala arg leu ala asn his
 121/41 151/51
 CTG GTC GAT CAG GGG TGC GAC GGT CTG GTG GTC TCG GGC ACC ACC GGC GAG TCG CCG ACC
 leu val asp gln gly cys asp gly leu val val ser gly thr thr gly glu ser pro thr
 181/61 211/71
 ACC ACC GAC GGG GAG AAA ATC GAG CTG CTG CGG GCC GTC TTG GAA GCG GTG GGG GAC CGG
 thr thr asp gly glu lys ile glu leu leu arg ala val leu glu ala val gly asp arg
 241/81 271/91
 GCC CGT GTT ATC GCC GGT GCC GGC ACC TAT GAC ACC GCG CAC AGC ATC CGG CTG GCC AAG
 ala arg val ile ala gly ala gly thr tyr asp thr ala his ser ile arg leu ala lys
 301/101 331/111
 GCT TGT GCG GCC GAG GGT GCG CAC GGG CTG CTG GTG GTC ACG CCC TAC TAT TCC AAG CCG
 ala cys ala ala glu gly ala his gly leu leu val val thr pro tyr tyr ser lys pro
 361/121 391/131
 CCG CAG CGG GGG CTG CAA GCC CAT TTC ACC GCC GTC GCC GAC GCG ACC GAG CTG CCG ATG
 pro gln arg gly leu gln ala his phe thr ala val ala asp ala thr glu leu pro met
 421/141 451/151
 CTG CTC TAT GAC ATC CCG GGG CGG TCG GCG GTG CCG ATC GAG CCC GAC ACG ATC CGC GCG
 leu leu tyr asp ile pro gly arg ser ala val pro ile glu pro asp thr ile arg ala
 481/161 511/171
 TTG GCG TCG CAT CCG AAC ATC GTC GGA GTC AAG GAC GCC AAA GCC GAC CTG CAC AGC GGC
 leu ala ser his pro asn ile val gly val lys asp ala lys ala asp leu his ser gly
 541/181 571/191
 GCC CAA ATC ATG GCC GAC ACC GGA CTG GCC TAC TAT TCC GGC GAC GAC GCG CTC AAC CTG
 ala gln ile met ala asp thr gly leu ala tyr tyr ser gly asp asp ala leu asn leu
 601/201 631/211
 CCC TGG CTG GCC ATG GGC GCC ACG GGC TTC ATC AGC GTG ATT GCC CAC CTG GCA GCC GGG
 pro trp leu ala met gly ala thr gly phe ile ser val ile ala his leu ala ala gly
 661/221 691/231
 CAG CTT CGA GAG TTG TTG TCC GCC TTC GGT TCT GGG GAT ATC GCC ACC GCC CGC AAG ATC
 gln leu arg glu leu leu ser ala phe gly ser gly asp ile ala thr ala arg lys ile
 721/241 751/251
 AAC ATT GCG GTC GCC CCG CTG TGC AAC GCG ATG AGC CGC CTG GGT GGG GTG ACG TTG TCC
 asn ile ala val ala pro leu cys asn ala met ser arg leu gly gly val thr leu ser
 781/261 811/271
 AAG GCG GGC TTG CGG CTG CAG GGC ATC GAC GTC GGT GAT CCC CGG CTG CCC CAG GTG GCC
 lys ala gly leu arg leu gln gly ile asp val gly asp pro arg leu pro gln val ala
 841/281 871/291
 GCG ACA CCG GAG CAG ATC GAC GCG TTG GCC GCC GAC ATG CGC GCG GCC TCG GTG CTT CGG
 ala thr pro glu gln ile asp ala leu ala ala asp met arg ala ala ser val leu arg)

901/301
 TGA
 OPA

SEQ ID NOS: 629-630

FIGURE 37D

ORF according to Cole et al., 1998 (Nature 393 537-544) containing Rv2753c

SEQ ID NO: 631
1/1

31/11

TAA GGT GAG CGC CGT GGC CGA GAC CGC GCC GCT GCG CGT GCA ACT GAT CGC CAA GAC CGA
OCH (gly glu arg arg gly arg asp arg ala ala ala arg ala thr asp arg gln asp arg
61/21) SEQ ID NO: 632 91/31
CTT CTT GGC CCC ACC CGA CGT GCC CTG GAC CAC CGA CGC CGA CGG CGG ACC CGC GCT GGT
leu leu gly pro thr arg arg ala leu asp his arg arg arg arg arg thr arg ala gly
121/41 151/51
CGA GTT CGC CGG CCG GGC CTG CTA TCA GAG CTG GTC CAA GCC CAA TCC CAA GAC CGC CAC
arg val arg arg pro gly leu leu ser glu leu val gln ala gln ser gln asp arg his
181/61 211/71
CAA CGC CGG CTA CCT CCG GCA CAT CAT CGA CGT CGG ACA TTT CTC GGT GCT AGA GCA TGC
gln arg arg leu pro pro ala his his arg arg arg thr phe leu gly ala arg ala cys
241/81 271/91
CAG CGT GTC GTT CTA CAT CAC CGG GAT CTC GCG ATC GTG CAC CCA CGA GCT GAT CCG CCA
gln arg val val leu his his arg asp leu ala ile val his pro arg ala asp pro pro
301/101 331/111
CCG GCA TTT CTC CTA CTC GCA GCT CTC CCA GCG CTA CGT ACC CGA GAA GGA CTC GCG GGT
pro ala phe leu leu leu ala ala leu pro ala leu arg thr arg glu gly leu ala gly
361/121 391/131
CGT CGT GCC GCC CGG CAT GGA GGA CGA CGC CGA CCT GCG CCA CAT CCT GAC CGA GGC CGC
arg arg ala ala arg his gly gly arg arg arg pro ala pro his pro asp arg gly arg
421/141 451/151
CGA CGC CGC CCG CGC CAC CTA CAG CGA GCT GCT GGC CAA GCT GGA AGC CAA GTT CGC CGA
arg arg arg pro arg his leu gln arg ala ala gly gln ala gly ser gln val arg arg
481/161 511/171
CCA ACC CAA CGC GAT CCT GCG CCG CAA GCA GGC CCG CCA AGC CGC CCG CGC GGT GCT GCC
pro thr gln arg asp pro ala pro gln ala gly pro pro ser arg pro arg gly ala ala
541/181 571/191
CAA CGC CAC CGA AAC CCG CAT CGT GGT GAC CGG CAA CTA CCG GGC CTG GCG GCA CTT CAT
gln arg his arg asn pro his arg gly asp arg gln leu pro gly leu ala ala leu his
601/201 631/211
CGC AAT GCG GGC CAG CGA GCA CGC CGA CGT GGA AAT CCG GCG ACT GGC CAT CGA ATG CCT
arg asn ala gly gln arg ala arg arg arg gly asn pro ala thr gly his arg met pro
661/221 691/231
GCG CCA GCT CGC CGC CGT GGC CCC CGC GGT GTT CGC CGA CTT CGA GGT GAC CAC CCT GGC
ala pro ala arg arg arg gly pro arg gly val arg arg leu arg gly asp his pro gly
721/241 751/251
CGA CGG CAC CGA GGT GGC GAC CAG CCC GTT GGC GAC CGA AGC CTG AGG CGG CGT GTC GCT
arg arg his arg gly gly asp gln pro val gly asp arg ser leu arg arg arg val ala
781/261 811/271
GGA CAA ACA CGC GCG CTC GCG GCC GGG ATA AAG CGC CAG GTA ACC TTG GGA GCC GTG ACC
gly gln thr arg ala leu ala ala gly ile lys arg gln val thr leu gly ala val thr
841/281 871/291
ACC GTC GGA TTC GAC GTC GCA GCG CGC CTA GGA ACC CTG CTG ACC GCG ATG GTG ACA CCG
thr val gly phe asp val ala ala arg leu gly thr leu leu thr ala met val thr pro
901/301 931/311
TTT AGC GGC GAT GGC TCC CTG GAC ACC GCC ACC GCG GCG CGG CTG GCC AAC CAC CTG GTC
phe ser gly asp gly ser leu asp thr ala thr ala ala arg leu ala asn his leu val
961/321 991/331
GAT CAG GGG TGC GAC GGT CTG GTG GTC TCG GGC ACC ACC GGC GAG TCG CCG ACC ACC ACC
asp gln gly cys asp gly leu val val ser gly thr thr gly glu ser pro thr thr thr

SEQ ID NOS: 631-682

FIGURE 37E

1021/341	1051/351
GAC GGG GAG AAA ATC GAG CTG CTG CGG GCC	GTC TTG GAA GCG GTG GGG GAC CGG GCC CGT
asp gly glu lys ile glu leu leu arg ala	val leu glu ala val gly asp arg ala arg
1081/361	1111/371
GTT ATC GCC GGT GCC GGC ACC TAT GAC ACC	GCG CAC AGC ATC CGG CTG GCC AAG GCT TGT
val ile ala gly ala gly thr tyr asp thr	ala his ser ile arg leu ala lys ala cys
1141/381	1171/391
GCG GCC GAG GGT GCG CAC GGG CTG CTG GTG	GTC ACG CCC TAC TAT TCC AAG CCG CCG CAG
ala ala glu gly ala his gly leu leu val	val thr pro tyr tyr ser lys pro pro gln
1201/401	1231/411
CGG GGG CTG CAA GCC CAT TTC ACC GCC GTC	GCC GAC GCG ACC GAG CTG CCG ATG CTG CTC
arg gly leu gln ala his phe thr ala val	ala asp ala thr glu leu pro met leu leu
1261/421	1291/431
TAT GAC ATC CCG GGG CGG TCG GCG GTG CCG	ATC GAG CCC GAC ACG ATC CGC GCG TTG GCG
tyr asp ile pro gly arg ser ala val pro	ile glu pro asp thr ile arg ala leu ala
1321/441	1351/451
TCG CAT CCG AAC ATC GTC GGA GTC AAG GAC	GCC AAA GCC GAC CTG CAC AGC GGC GCC CAA
ser his pro asn ile val gly val lys asp	ala lys ala asp leu his ser gly ala gln
1381/461	1411/471
ATC ATG GCC GAC ACC GGA CTG GCC TAC TAT	TCC GGC GAC GAC GCG CTC AAC CTG CCC TGG
ile met ala asp thr gly leu ala tyr tyr	ser gly asp asp ala leu asn leu pro trp
1441/481	1471/491
CTG GCC ATG GGC GCC ACG GGC TTC ATC AGC	GTG ATT GCC CAC CTG GCA GCC GGG CAG CTT
leu ala met gly ala thr gly phe ile ser	val ile ala his leu ala ala gly gln leu
1501/501	1531/511
CGA GAG TTG TTG TCC GCC TTC GGT TCT GGG	GAT ATC GCC ACC GCC CGC AAG ATC AAC ATT
arg glu leu leu ser ala phe gly ser gly	asp ile ala thr ala arg lys ile asn ile
1561/521	1591/531
GCG GTC GCC CCG CTG TGC AAC GCG ATG AGC	CGC CTG GGT GGG GTG ACG TTG TCC AAG GCG
ala val ala pro leu cys asn ala met ser	arg leu gly gly val thr leu ser lys ala
1621/541	1651/551
GGC TTG CGG CTG CAG GGC ATC GAC GTC GGT	GAT CCC CGG CTG CCC CAG GTG GCC GCG ACA
gly leu arg leu gln gly ile asp val gly	asp pro arg leu pro gln val ala ala thr
1681/561	1711/571
CCG GAG CAG ATC GAC GCG TTG GCC GCC GAC	ATG CGC GCG GCC TCG GTG CTT CGG TGA
pro glu gln ile asp ala leu ala ala asp	met arg ala ala ser val leu arg)OPA

SEQ ID NDS: 631-632

FIGURE 37E (continued 1)

SEQ ID NO: 633

1/1 31/11
 GCG GTG AAC TGG TGG GCC CGG ATG GTT CAA GTA CGC CGT CGC AAA CTC GAG CAC AAC AGG
 ala val asn trp trp ala arg met val gln val arg arg arg lys leu glu his asn arg
 61/21 91/31
 AGA CGA CGG ATG GAA GGA GAT GCT GGC GCC GGC CAG CTG AAC CCT GCC GAT GCG AAT AAG
 arg arg arg met glu gly asp ala gly ala gly gln leu asn pro ala asp ala asn lys
 121/41 151/51
 TCG TCG TCT ACG GAG GTG AAG GCG GCG GAT TCG GCG GAA TCT GAC GCC GGA GCC GAC CAG
 ser ser ser thr glu val lys ala ala asp ser ala glu ser asp ala gly ala asp gln
 181/61 211/71
 ACT GGC CCG CAG GTG AAG GCG GCG GAT TCG GCG GAA TCT GAC GCC GGA GAG CTC GGC GAG
 thr gly pro gln val lys ala ala asp ser ala glu ser asp ala gly glu leu gly glu
 241/81 271/91
 GAC GCG TGC CCA GAA CAG GCC CTC GTC GAG CGG CGC CCG TCG CGG TTG CGG CGA GGC TGG
 asp ala cys pro glu gln ala leu val glu arg arg pro ser arg leu arg arg gly trp
 301/101 331/111
 CTT GTT GGC ATT GCG GCG ACG CTG CTC GCG TTG GCC GGT GGC CTT GGC GCA GCG GGT TAT
 leu val gly ile ala ala thr leu leu ala leu ala gly gly leu gly ala ala gly tyr
 361/121 391/131
 TTT GCG TTG CGC TCA CAC CAG GAA AGC CAA TCA ATC GCG CGC GAG GAC CTT GCG GCC ATT
 phe ala leu arg ser his gln glu ser gln ser ile ala arg glu asp leu ala ala ile
 421/141 451/151
 GAG GCC GCT AAG GAT TGC GTT GCG GCC ACG CAG GCA CCC GAT GCT GGG GCG ATG TCG GCT
 glu ala ala lys asp cys val ala ala thr gln ala pro asp ala gly ala met ser ala
 481/161
 AGC ATG CAG AAG ATC
 ser met gln lys ile)

SEQ ID NOS: 633-634

FIGURE 38A

SEQ ID NO: 635

1/1 31/11
 CAG CGG TGA ACT GGT GGG CCC GGA TGG TTC AAG TAC GCC GTC GCA AAC TCG AGC ACA ACA
 gln arg OPA (thr gly gly pro gly trp phe lys tyr ala val ala asn ser ser thr thr
 61/21 91/31
 GGA GAC GAC GGA TGG AAG GAG ATG CTG GCG CCG GCC AGC TGA ACC CTG CCG ATG CGA ATA
 gly asp asp gly trp lys glu met leu ala pro ala ser) OPA (thr leu pro met arg ile
 121/41 151/51
 AGT CGT CGT CTA CGG AGG TGA AGG CGG CGG ATT CGG CGG AAT CTG ACG CCG GAG CCG ACC
 ser arg arg leu arg arg) OPA (arg arg arg ile arg arg asn leu thr pro glu pro thr
 181/61 211/71
 AGA CTG GCC CGC AGG TGA AGG CGG CGG ATT CGG CGG AAT CTG ACG CCG GAG AGC TCG GCG
 arg leu ala arg arg) OPA (arg arg arg ile arg arg asn leu thr pro glu ser ser ala
 241/81 271/91
 AGG ACG CGT GCC CAG AAC AGG CCC TCG TCG AGC GGC GCC CGT CGC GGT TGC GGC GAG GCT
 arg thr arg ala gln asn arg pro ser ser ser gly ala arg arg gly cys gly glu ala
 301/101 331/111
 GGC TTG TTG GCA TTG CGG CGA CGC TGC TCG CGT TGG CCG GTG GCC TTG GCG CAG CGG GTT
 gly leu leu ala leu arg arg arg cys ser arg trp pro val ala leu ala gln arg val
 361/121 391/131
 ATT TTG CGT TGC GCT CAC ACC AGG AAA GCC AAT CAA TCG CGC GCG AGG ACC TTG CGG CCA
 ile leu arg cys ala his thr arg lys ala asn gln ser arg ala arg thr leu arg pro
 421/141 451/151
 TTG AGG CCG CTA AGG ATT GCG TTG CGG CCA CGC AGG CAC CCG ATG CTG GGG CGA TGT CGG
 leu arg pro leu arg ile ala leu arg pro arg arg his pro met leu gly arg cys arg
 481/161
 CTA GCA TGC AGA AGA TC
 leu ala cys arg arg)

SEQ ID NOS: 635-639

FIGURE 38B

SEQ ID NO: 641
 1/1
 AGC GGT GAA CTG GTG GGC CCG GAT GGT TCA AGT ACG CCG TCG CAA ACT CGA GCA CAA CAG
 (ser gly glu leu val gly pro asp gly ser ser thr pro ser gln thr arg ala gln gln
 61/21
 GAG ACG ACG GAT GGA AGG AGA TGC TGG CGC CGG CCA GCT GAA CCC TGC CGA TGC GAA TAA
 glu thr thr asp gly arg arg cys trp arg arg pro ala glu pro cys arg cys glu) OCH
 121/41
 GTC GTC GTC TAC GGA GGT GAA GGC GGC GGA TTC GGC GGA ATC TGA CGC CGG AGC CGA CCA
 (val val val tyr gly gly glu gly gly gly phe gly gly ile) OPA (arg arg ser arg pro
 181/61
 GAC TGG CCC GCA GGT GAA GGC GGC GGA TTC GGC GGA ATC TGA CGC CGG AGA GCT CGG CGA
 asp trp pro ala gly glu gly gly gly phe gly gly ile) OPA (arg arg arg ala arg arg
 241/81
 GGA CGC GTG CCC AGA ACA GGC CCT CGT CGA GCG GCG CCC GTC GCG GTT GCG GCG AGG CTG
 gly arg val pro arg thr gly pro arg arg ala ala pro val ala val ala ala arg leu
 301/101
 GCT TGT TGG CAT TGC GGC GAC GCT GCT CGC GTT GGC CGG TGG CCT TGG CGC AGC GGG TTA
 ala cys trp his cys gly asp ala ala arg val gly arg trp pro trp arg ser gly leu
 361/121
 TTT TGC GTT GCG CTC ACA CCA GGA AAG CCA ATC AAT CGC GCG CGA GGA CCT TGC GGC CAT
 phe cys val ala leu thr pro gly lys pro ile asn arg ala arg gly pro cys gly his)
 421/141
 TGA GGC CGC TAA GGA TTG CGT TGC GGC CAC GCA GGC ACC CGA TGC TGG GGC GAT GTC GGC
 OPA gly arg OCH (gly leu arg cys gly his ala gly thr arg cys trp gly asp val gly)
 481/161
 TAG CAT GCA GAA GAT C
 AMB (his ala glu asp)
 ↳ SEQ ID NO: 646

SEQ ID NO: 642
 1/1
 AGC GGT GAA CTG GTG GGC CCG GAT GGT TCA AGT ACG CCG TCG CAA ACT CGA GCA CAA CAG
 (ser gly glu leu val gly pro asp gly ser ser thr pro ser gln thr arg ala gln gln
 61/21
 GAG ACG ACG GAT GGA AGG AGA TGC TGG CGC CGG CCA GCT GAA CCC TGC CGA TGC GAA TAA
 glu thr thr asp gly arg arg cys trp arg arg pro ala glu pro cys arg cys glu) OCH
 121/41
 GTC GTC GTC TAC GGA GGT GAA GGC GGC GGA TTC GGC GGA ATC TGA CGC CGG AGC CGA CCA
 (val val val tyr gly gly glu gly gly gly phe gly gly ile) OPA (arg arg ser arg pro
 181/61
 GAC TGG CCC GCA GGT GAA GGC GGC GGA TTC GGC GGA ATC TGA CGC CGG AGA GCT CGG CGA
 asp trp pro ala gly glu gly gly gly phe gly gly ile) OPA (arg arg arg ala arg arg
 241/81
 GGA CGC GTG CCC AGA ACA GGC CCT CGT CGA GCG GCG CCC GTC GCG GTT GCG GCG AGG CTG
 gly arg val pro arg thr gly pro arg arg ala ala pro val ala val ala ala arg leu
 301/101
 GCT TGT TGG CAT TGC GGC GAC GCT GCT CGC GTT GGC CGG TGG CCT TGG CGC AGC GGG TTA
 ala cys trp his cys gly asp ala ala arg val gly arg trp pro trp arg ser gly leu
 361/121
 TTT TGC GTT GCG CTC ACA CCA GGA AAG CCA ATC AAT CGC GCG CGA GGA CCT TGC GGC CAT
 phe cys val ala leu thr pro gly lys pro ile asn arg ala arg gly pro cys gly his)
 421/141
 TGA GGC CGC TAA GGA TTG CGT TGC GGC CAC GCA GGC ACC CGA TGC TGG GGC GAT GTC GGC
 OPA gly arg OCH (gly leu arg cys gly his ala gly thr arg cys trp gly asp val gly)
 481/161
 TAG CAT GCA GAA GAT C
 AMB (his ala glu asp)
 ↳ SEQ ID NO: 645

SEQ ID NOS: 640-646

FIGURE 38C

122/185

Sequence Rv0175 predicted by Cole et al., 1998 (Nature 393 537-544) and containing seq38A

1/1 31/11
 GTG AAG GCG GCG GAT TCG GCG GAA TCT GAC GCC GGA GCC GAC CAG ACT GGC CCG CAG GTG
 val lys ala ala asp ser ala glu ser asp ala gly ala asp gln thr gly pro gln val
 61/21 91/31
 AAG GCG GCG GAT TCG GCG GAA TCT GAC GCC GGA GAG CTC GGC GAG GAC GCG TGC CCA GAA
 lys ala ala asp ser ala glu ser asp ala gly glu leu gly glu asp ala cys pro glu
 121/41 151/51
 CAG GCC CTC GTC GAG CGG CGC CCG TCG CGG TTG CGG CGA GGC TGG CTT GTT GGC ATT GCG
 gln ala leu val glu arg arg pro ser arg leu arg arg gly trp leu val gly ile ala
 181/61 211/71
 GCG ACG CTG CTC GCG TTG GCC GGT GGC CTT GGC GCA GCG GGT TAT TTT GCG TTG CGC TCA
 ala thr leu leu ala leu ala gly gly leu gly ala ala gly tyr phe ala leu arg ser
 241/81 271/91
 CAC CAG GAA AGC CAA TCA ATC GCG CGC GAG GAC CTT GCG GCC ATT GAG GCC GCT AAG GAT
 his gln glu ser gln ser ile ala arg glu asp leu ala ala ile glu ala ala lys asp
 301/101 331/111
 TGC GTT GCG GCC ACG CAG GCA CCC GAT GCT GGG GCG ATG TCG GCT AGC ATG CAG AAG ATC
 cys val ala ala thr gln ala pro asp ala gly ala met ser ala ser met gln lys ile
 361/121 391/131
 ATC GAG TGT GGC ACC GGT GAT TTC GGT GCC CAG GCG TCG TTG TAC ACC AGC ATG CTC GTC
 ile glu cys gly thr gly asp phe gly ala gln ala ser leu tyr thr ser met leu val
 421/141 451/151
 GAG GCG TAT CAA GCG GCC AGC GTC CAC GTG CAA GTG ACC GAT ATG CGC GCG GCG GTC GAG
 glu ala tyr gln ala ala ser val his val gln val thr asp met arg ala ala val glu
 481/161 511/171
 CGC AAC AAC AAT GAC GGG TCG GTC GAT GTT CTG GTG GCG CTC CGG GTC AAG GTG TCC AAC
 arg asn asn asn asp gly ser val asp val leu val ala leu arg val lys val ser asn
 541/181 571/191
 ACC GAC TCG GAT GCC CAT GAA GTC GGC TAC CGT CTT CGG GTC CGG ATG GCA CTG GAT GAG
 thr asp ser asp ala his glu val gly tyr arg leu arg val arg met ala leu asp glu
 601/201 631/211
 GGC CGC TAT AAG ATC GCC AAA CTC GAC CAG GTG ACG AAG TGA
 gly arg tyr lys ile ala lys leu asp gln val thr lys)OPA

SEQ ID NOS: 647-648

FIGURE 38D

SEQ ID NO: 649

ORF according to Cole et al., 1998 (Nature 393 537-544) containing Rv0175

1/1

31/11

(TGA ACT GGT GGG GCC GGA TGG TGT CAA GTA CGC CGT CGC AAA CTC GAG CAC AAC AGG AGA
 OPA(thr gly gly ala gly trp cys gln val arg arg arg lys leu glu his asn arg arg
 61/21) ^{SEQ ID NO: 650}
 CGA CGG ATG GAA GGA GAT GCT GGC GCC GGC CAG CTG AAC CCT GCC GAT GCG AAT AAG TCG
 arg arg met glu gly asp ala gly ala gly gln leu asn pro ala asp ala asn lys ser
 121/41
 TCG TCT ACG GAG GTG AAG GCG GCG GAT TCG GCG GAA TCT GAC GCC GGA GCC GAC CAG ACT
 ser ser thr glu val lys ala ala asp ser ala glu ser asp ala gly ala asp gln thr
 181/61
 GGC CCG CAG GTG AAG GCG GCG GAT TCG GCG GAA TCT GAC GCC GGA GAG CTC GGC GAG GAC
 gly pro gln val lys ala ala asp ser ala glu ser asp ala gly glu leu gly glu asp
 241/81
 GCG TGC CCA GAA CAG GCC CTC GTC GAG CGG CGC CCG TCG CGG TTG CGG CGA GGC TGG CTT
 ala cys pro glu gln ala leu val glu arg arg pro ser arg leu arg arg gly trp leu
 301/101
 GTT GGC ATT GCG GCG ACG CTG CTC GCG TTG GCC GGT GGC CTT GGC GCA GCG GGT TAT TTT
 val gly ile ala ala thr leu leu ala leu ala gly gly leu gly ala ala gly tyr phe
 361/121
 GCG TTG CGC TCA CAC CAG GAA AGC CAA TCA ATC GCG CGC GAG GAC CTT GCG GCC ATT GAG
 ala leu arg ser his gln glu ser gln ser ile ala arg glu asp leu ala ala ile glu
 421/141
 GCC GCT AAG GAT TGC GTT GCG GCC ACG CAG GCA CCC GAT GCT GGG GCG ATG TCG GCT AGC
 ala ala lys asp cys val ala ala thr gln ala pro asp ala gly ala met ser ala ser
 481/161
 ATG CAG AAG ATC ATC GAG TGT GGC ACC GGT GAT TTC GGT GCC CAG GCG TCG TTG TAC ACC
 met gln lys ile ile glu cys gly thr gly asp phe gly ala gln ala ser leu tyr thr
 541/181
 AGC ATG CTC GTC GAG GCG TAT CAA GCG GCC AGC GTC CAC GTG CAA GTG ACC GAT ATG CGC
 ser met leu val glu ala tyr gln ala ala ser val his val gln val thr asp met arg
 601/201
 GCG GCG GTC GAG CGC AAC AAC AAT GAC GGG TCG GTC GAT GTT CTG GTG GCG CTC CGG GTC
 ala ala val glu arg asn asn asn asp gly ser val asp val leu val ala leu arg val
 661/221
 AAG GTG TCC AAC ACC GAC TCG GAT GCC CAT GAA GTC GGC TAC CGT CTT CGG GTC CGG ATG
 lys val ser asn thr asp ser asp ala his glu val gly tyr arg leu arg val arg met
 721/241
 GCA CTG GAT GAG GGC CGC TAT AAG ATC GCC AAA CTC GAC CAG GTG ACG AAG TGA
 ala leu asp glu gly arg tyr lys ile ala lys leu asp gln val thr lys)OPA

SEQ ID NOS: 649-650

FIGURE 38E

124/185

SEQ ID NO: 651

1/1 31/11
ACAC CCT CCC CCC CCG CCG CCG CTG CCG CCG GTT CCC TTT CCC AAG GAA TGT CCG GCG CCG
thr pro pro pro pro pro pro leu pro pro val pro phe pro lys glu cys pro ala pro
61/21 91/31
GGC GTG ATG CAA GGC TGC CTT GAG AGC ACC AGC GGC TTG ATC ATG GGC ATC GAC AGC AAG
gly val met gln gly cys leu glu ser thr ser gly leu ile met gly ile asp ser lys
121/41 151/51
ACC GCA CTG GTC GCC GAG CGC ATC ACC GGT GCC GTC GAG GAG ATC
thr ala leu val ala glu arg ile thr gly ala val glu glu ile)

SEQ ID NOS: 651-652

FIGURE 39A

SEQ ID NO: 653

1/1 31/11
CAC CTC CCC CCC CGC CGC CGC TGC CGC CGG TTC CCT TTC CCA AGG AAT GTC CGG CGC CGG
(his leu pro pro arg arg arg cys arg arg phe pro phe pro arg asn val arg arg arg
61/21 91/31
GCG TGA TGC AAG GCT GCC TTG AGA GCA CCA GCG GCT TGA TCA TGG GCA TCG ACA GCA AGA
ala) OPA (cys lys ala ala leu arg ala pro ala ala) OPA (ser trp ala ser thr ala arg
121/41 151/51
CCG CAC TGG TCG CCG AGC GCA TCA CCG GTG CCG TCG AGG AGA TC
pro his trp ser pro ser ala ser pro val pro ser arg arg)

SEQ ID NOS: 653-656

FIGURE 39B

SEQ ID NO: 657

1/1 31/11
GAC ACC TCC CCC CCC GCC GCC GCT GCC GCC GGT TCC CTT TCC CAA GGA ATG TCC GGC GCC
(asp thr ser pro pro ala ala ala ala ala gly ser leu ser gln gly met ser gly ala
61/21 91/31
GGG CGT GAT GCA AGG CTG CCT TGA GAG CAC CAG CGG CTT GAT CAT GGG CAT CGA CAG CAA
gly arg asp ala arg leu pro) OPA (glu his gln arg leu asp his gly his arg gln gln
121/41 151/51
GAC CGC ACT GGT CGC CGA GCG CAT CAC CGG TGC CGT CGA GGA GAT C
asp arg thr gly arg arg ala his his arg cys arg arg gly asp)

SEQ ID NOS: 657-659

FIGURE 39C

Coding sequence Rv3006 predicted by Cole et al., 1998 (Nature 393 537-544) and containing seq39A

1/1
 ATG TGG ACA ACG CGG TTG GTT CGA TCC GGA CTC GCC GCG CTG TGC GCG GCA GTG CTG GTA
 Met trp thr thr arg leu val arg ser gly leu ala ala leu cys ala ala val leu val
 61/21
 TCG AGC GGC TGC GCA CGG TTC AAC GAC GCT CAA TCT CAG CCG TTC ACC ACC GAA CCG GAG
 ser ser gly cys ala arg phe asn asp ala gln ser gln pro phe thr thr glu pro glu
 121/41
 CTG CGG CCC CAA CCC AGC TCG ACA CCT CCC CCC CCG CCG CCG CTG CCG CCG GTT CCC TTT
 leu arg pro gln pro ser ser thr pro pro pro pro pro pro leu pro pro val pro phe
 181/61
 CCC AAG GAA TGT CCG GCG CCG GGC GTG ATG CAA GGC TGC CTT GAG AGC ACC AGC GGC TTG
 pro lys glu cys pro ala pro gly val met gln gly cys leu glu ser thr ser gly leu
 241/81
 ATC ATG GGC ATC GAC AGC AAG ACC GCA CTG GTC GCC GAG CGC ATC ACC GGT GCC GTC GAG
 ile met gly ile asp ser lys thr ala leu val ala glu arg ile thr gly ala val glu
 301/101
 GAG ATC TCT ATC AGC GCC GAG CCG AAG GTA AAG ACG GTC ATC CCC GTG GAT CCT GCC GGT
 glu ile ser ile ser ala glu pro lys val lys thr val ile pro val asp pro ala gly
 361/121
 GAC GGT GGC TTG ATG GAC ATT GTG CTG TCG CCC ACC TAC TCG CAA GAC CGG CTG ATG TAC
 asp gly gly leu met asp ile val leu ser pro thr tyr ser gln asp arg leu met tyr
 421/141
 GCC TAC ATC AGC ACG CCC ACC GAC AAC CGG GTG GTG CGA GTG GCC GAC GGC GAC ATC CCC
 ala tyr ile ser thr pro thr asp asn arg val val arg val ala asp gly asp ile pro
 481/161
 AAG GAC ATC CTG ACC GGC ATC CCC AAA GGT GCT GCC GGT AAC ACC GGG GCG CTG ATC TTC
 lys asp ile leu thr gly ile pro lys gly ala ala gly asn thr gly ala leu ile phe
 541/181
 ACC AGT CCC ACC ACG CTG GTC GTG ATG ACC GGG GAT GCT GGC GAC CCG GCG TTG GCC GCC
 thr ser pro thr thr leu val val met thr gly asp ala gly asp pro ala leu ala ala
 601/201
 GAT CCC CAA TCG TTG GCC GGT AAG GTC CTG CGT ATC GAA CAG CCC ACC ACC ATC GGC CAG
 asp pro gln ser leu ala gly lys val leu arg ile glu gln pro thr thr ile gly gln
 661/221
 ACG CCG CCG ACG ACG GCG CTG TCT GGC ATC GGC TCC GGC GGC GGC TTG TGC ATC GAT CCG
 thr pro pro thr thr ala leu ser gly ile gly ser gly gly gly leu cys ile asp pro
 721/241
 GTC GAC GGC TCG CTA TAT GTC GCC GAC CGC ACG CCA ACG GCG GAC CGA TTG CAG CGC ATC
 val asp gly ser leu tyr val ala asp arg thr pro thr ala asp arg leu gln arg ile
 781/261
 ACC AAG AAC TCG GAG GTC TCT ACG GTA TGG ACC TGG CCG GAC AAG CCC GGC GTG GCC GGG
 thr lys asn ser glu val ser thr val trp thr trp pro asp lys pro gly val ala gly
 841/281
 TGT GCC GCG ATG GAC GGC ACC GTG CTG GTC AAC CTG ATT AAT ACC AAA CTG ACG GTG GCG
 cys ala ala met asp gly thr val leu val asn leu ile asn thr lys leu thr val ala
 901/301
 GTC CCG CTC GCG CCG TCG ACC GGT GCG GTC ACC GGA GAA CCC GAC GTT GTC CGC AAA GAC
 val arg leu ala pro ser thr gly ala val thr gly glu pro asp val val arg lys asp
 961/321
 ACT CAT GCG CAT GCG TGG GCA TTA CGG ATG TCG CCG GAC GGC AAC GTC TGG GGA GCC ACC
 thr his ala his ala trp ala leu arg met ser pro asp gly asn val trp gly ala thr
 1021/341
 GTC AAC AAG ACC GCC GGC GAC GCC GAG AAG CTC GAC GAT GTG GTG TTC CCG CTG TTC CCG
 val asn lys thr ala gly asp ala glu lys leu asp asp val val phe pro leu phe pro
 1081/361
 CAG GGT GGC GGC TTC CCG CGC AAC AAC GAC GAC AAG ACC TGA
 gln gly gly gly phe pro arg asn asn asp asp lys thr OPA

SEQ ID : NDS:660-661

FIGURE 39D

ORF according to Cole et al., 1998 (Nature 393 537-544) and containing Rv3006

1/1

31/11

TAA GGC CAT TTA GTG CCG AAT TGG GGA TTT GAG CGG CGC TTT CGC CAG ACA ATC CGC ACA
 OCH (gly his leu val pro asn trp gly phe glu arg arg phe arg gln thr ile arg thr
 61/211
 TTG ACC CTG ACC AGC CCA CCA AAA GGC CCC AAT TGG GCC GCC ATG CCG ACA GTG CGC ACC
 leu thr leu thr ser pro pro lys gly pro asn trp ala ala met pro thr val arg thr
 121/41
 CCG GCA GGT GGC GGC GAT GCC CAC AAT GTC CGT AGC CTG TCG GTC ATG TGG ACA ACG CGG
 pro ala gly gly gly asp ala his asn val arg ser leu ser val met trp thr thr arg
 181/61
 TTG GTT CGA TCC GGA CTC GCC GCG CTG TGC GCG GCA GTG CTG GTA TCG AGC GGC TGC GCA
 leu val arg ser gly leu ala ala leu cys ala ala val leu val ser ser gly cys ala
 241/81
 CGG TTC AAC GAC GCT CAA TCT CAG CCG TTC ACC ACC GAA CCG GAG CTG CGG CCC CAA CCC
 arg phe asn asp ala gln ser gln pro phe thr thr glu pro glu leu arg pro gln pro
 301/101
 AGC TCG ACA CCT CCC CCC CCG CCG CCG CTG CCG CCG GTT CCC TTT CCC AAG GAA TGT CCG
 ser ser thr pro pro pro pro pro pro leu pro pro val pro phe pro lys glu cys pro
 361/121
 GCG CCG GGC GTG ATG CAA GGC TGC CTT GAG AGC ACC AGC GGC TTG ATC ATG GGC ATC GAC
 ala pro gly val met gln gly cys leu glu ser thr ser gly leu ile met gly ile asp
 421/141
 AGC AAG ACC GCA CTG GTC GCC GAG CGC ATC ACC GGT GGC GTC GAG GAG ATC TCT ATC AGC
 ser lys thr ala leu val ala glu arg ile thr gly ala val glu glu ile ser ile ser
 481/161
 GCC GAG CCG AAG GTA AAG ACG GTC ATC CCC GTG GAT CCT GCC GGT GAC GGT GGC TTG ATG
 ala glu pro lys val lys thr val ile pro val asp pro ala gly asp gly gly leu met
 541/181
 GAC ATT GTG CTG TCG CCC ACC TAC TCG CAA GAC CGG CTG ATG TAC GCC TAC ATC AGC ACG
 asp ile val leu ser pro thr tyr ser gln asp arg leu met tyr ala tyr ile ser thr
 601/201
 CCC ACC GAC AAC CGG GTG GTG CGA GTG GCC GAC GGC GAC ATC CCC AAG GAC ATC CTG ACC
 pro thr asp asn arg val val arg val ala asp gly asp ile pro lys asp ile leu thr
 661/221
 GGC ATC CCC AAA GGT GCT GCC GGT AAC ACC GGG GCG CTG ATC TTC ACC AGT CCC ACC ACG
 gly ile pro lys gly ala ala gly asn thr gly ala leu ile phe thr ser pro thr thr
 721/241
 CTG GTC GTG ATG ACC GGG GAT GCT GGC GAC CCG GCG TTG GCC GCC GAT CCC CAA TCG TTG
 leu val val met thr gly asp ala gly asp pro ala leu ala ala asp pro gln ser leu
 781/261
 GCC GGT AAG GTC CTG CGT ATC GAA CAG CCC ACC ACC ATC GGC CAG ACG CCG CCG ACG ACG
 ala gly lys val leu arg ile glu gln pro thr thr ile gly gln thr pro pro thr thr
 841/281
 GCG CTG TCT GGC ATC GGC TCC GGC GGC GGC TTG TGC ATC GAT CCG GTC GAC GGC TCG CTA
 ala leu ser gly ile gly ser gly gly gly leu cys ile asp pro val asp gly ser leu
 901/301
 TAT GTC GCC GAC CGC ACG CCA ACG GCG GAC CGA TTG CAG CGC ATC ACC AAG AAC TCG GAG
 tyr val ala asp arg thr pro thr ala asp arg leu gln arg ile thr lys asn ser glu

SEQ ID NOS: 662-663

FIGURE 39E

127/185

961/321	991/331
GTC TCT ACG GTA TGG ACC TGG CCG GAC AAG	CCC GGC GTG GCC GGG TGT GCC GCG ATG GAC
val ser thr val trp thr trp pro asp lys	pro gly val ala gly cys ala ala met asp
1021/341	1051/351
GGC ACC GTG CTG GTC AAC CTG ATT AAT ACC	AAA CTG ACG GTG GCG GTC CGG CTC GCG CCG
gly thr val leu val asn leu ile asn thr	lys leu thr val ala val arg leu ala pro
1081/361	1111/371
TCG ACC GGT GCG GTC ACC GGA GAA CCC GAC	GTT GTC CGC AAA GAC ACT CAT GCG CAT GCG
ser thr gly ala val thr gly glu pro asp	val val arg lys asp thr his ala his ala
1141/381	1171/391
TGG GCA TTA CGG ATG TCG CCG GAC GGC AAC	GTC TGG GGA GCC ACC GTC AAC AAG ACC GCC
trp ala leu arg met ser pro asp gly asn	val trp gly ala thr val asn lys thr ala
1201/401	1231/411
GGC GAC GCC GAG AAG CTC GAC GAT GTG GTG	TTC CCG CTG TTC CCG CAG GGT GGC GGC TTC
gly asp ala glu lys leu asp asp val val	phe pro leu phe pro gln gly gly gly phe
1261/421	
CCG CGC AAC AAC GAC GAC AAG ACC TGA	
pro arg asn asn asp asp lys thr	OPA

SEQ ID NDS: 662-663

FIGURE 39E (continued)

SEQ ID NO: 664

1/1	31/11
GAA GGC CTT GTT GAG CCG GCG CAC GAA AAC	GAT CGT TGT GTG TAC ATT GGT GTG TAT GGC
(glu gly leu val glu pro ala his glu asn	asp arg cys val tyr ile gly val tyr gly
61/21	91/31
TCG GTT GAA CGT GTA TGT GCC CGA CGA ATT	GGC GGA GCG CGC CAG GGC GCG GGG CTT GAA
ser val glu arg val cys ala arg arg ile	gly gly ala arg gln gly ala gly leu glu
121/41	151/51
CGT CTC GGC GCT GAC TCA GGC CGC GAT CAG	TGC CGA GTT GGA GAA CTC CGC AAC CGA TGC
arg leu gly ala asp ser gly arg asp gln	cys arg val gly glu leu arg asn arg cys
181/61	211/71
GTG GCT TGA GGG GTT GGA ACC CAG AAG CAC	CGG CGC TCG GCA TGA TGA CGT GCT GGG TGC
val ala) OPA (gly val gly thr gln lys his	arg arg ser ala) OPA (OPA arg ala gly cys
241/81	271/91
GAT CGA TGC CGC TCG CGA TGA GTT CGA AGC	GTG AGA GCA TCG CCC ACT TCG CCG CCG GAG
asp arg cys arg ser arg) OPA (val arg ser	val arg ala ser pro thr ser pro pro glu
301/101	331/111
CAG GTG GTC GTC GAC GCG AGT GCC ATG GTG	GAT C
gln val val val asp ala ser ala met val	asp)

SEQ ID NO: 665

SEQ ID NO: 931

SEQ ID NO: 932

SEQ ID NO: 933

SEQ ID NDS: 664-665, 931-933

FIGURE 40A

128/185

SEQ ID NO: 666
SEQ ID NO: 667

1/1 31/11
AAG GCC TTG TTG AGC CGG CGC ACG AAA ACG ATC GTT GTG TGT ACA TTG GTG TGT ATG GCT
lys ala leu leu ser arg arg thr lys thr ile val val cys thr leu val cys met ala
61/21 91/31
CGG TTG AAC GTG TAT GTG CCC GAC GAA TTG GCG GAG CGC GCC AGG GCG CGG GGC TTG AAC
arg leu asn val tyr val pro asp glu leu ala glu arg ala arg ala arg gly leu asn
121/41 151/51
GTC TCG GCG CTG ACT CAG GCC GCG ATC AGT GCC GAG TTG GAG AAC TCC GCA ACC GAT GCG
val ser ala leu thr gln ala ala ile ser ala glu leu glu asn ser ala thr asp ala
181/61 211/71
TGG CTT GAG GGG TTG GAA CCC AGA AGC ACC GGC GCT CGG CAT GAT GAC GTG CTG GGT GCG
trp leu glu gly leu glu pro arg ser thr gly ala arg his asp asp val leu gly ala
241/81 271/91
ATC GAT GCC GCT CGC GAT GAG TTC GAA GCG TGA GAG CAT CGC CCA CTT CGC CGC CGG AGC
ile asp ala ala arg asp glu phe glu ala) OPA (gly his arg pro leu arg arg arg ser
301/101 331/111
AGG TGG TCG TCG ACG CGA GTG CCA TGG TGG ATC
arg trp ser ser thr arg val pro trp trp ile)

SEQ ID NO: 668

SEQ ID NOS: 666-668

FIGURE 40B

SEQ ID NO: 669

1/1 31/11
AGG CCT TGT TGA GCC GGC GCA CGA AAA CGA TCG TTG TGT GTA CAT TGG TGT GTA TGG CTC
arg pro cys OPA (ala gly ala arg lys arg ser leu cys val his trp cys val trp leu
61/21 91/31
GGT TGA ACG TGT ATG TGC CCG ACG AAT TGG CGG AGC GCG CCA GGG CGC GGG GCT TGA ACG
gly) OPA (thr cys met cys pro thr asn trp arg ser ala pro gly arg gly ala) OPA (thr
121/41 151/51
TCT CGG CGC TGA CTC AGG CCG CGA TCA GTG CCG AGT TGG AGA ACT CCG CAA CCG ATG CGT
ser arg arg) OPA (leu arg pro arg ser val pro ser trp arg thr pro gln pro met arg
181/61 211/71
GGC TTG AGG GGT TGG AAC CCA GAA GCA CCG GCG CTC GGC ATG ATG ACG TGC TGG GTG CGA
gly leu arg gly trp asn pro glu ala pro ala leu gly met met thr cys trp val arg
241/81 271/91
TCG ATG CCG CTC GCG ATG AGT TCG AAG CGT GAG AGC ATC GCC CAC TTC GCC GCC GGA GCA
ser met pro leu ala met ser ser lys arg glu ser ile ala his phe ala ala gly ala
301/101
GGT GGT CGT CGA CGC GAG TGC CAT GGT GGA TC
gly gly arg arg arg glu cys his gly gly)

SEQ ID NO: 670

SEQ ID NO: 671

SEQ ID NO: 673

SEQ ID NO: 672

SEQ ID NOS: 669-673

FIGURE 40C

129/185

Coding sequence Rv0549c predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq40A

1/1 31/11
gtg aga gca tcg ccc act tcg ccg ccg gag cag gtg gtc gtc gac gcg agt gcc atg gtg
val arg ala ser pro thr ser pro pro glu gln val val val asp ala ser ala met val
61/21 91/31
gat cta ctg gct cgc act agc gat ccg tgc tct gcg gtg cgc gcg ccg ctg gct ccg acc
asp leu leu ala arg thr ser asp arg cys ser ala val arg ala arg leu ala arg thr
121/41 151/51
gcg atg cac gcg ccg gcg cac ttc gat gca gag gtg ttg tcg gcg ctg ggg cgc atg cag
ala met his ala pro ala his phe asp ala glu val leu ser ala leu gly arg met gln
181/61 211/71
cgc gcc ggc gca ctc acc gtt gcc tat gtc gat gcg gca ctg gag gag ttg cga cag gtg
arg ala gly ala leu thr val ala tyr val asp ala ala leu glu glu leu arg gln val
241/81 271/91
ccg gtg act cga cac ggt ctt tcg tcg ctg ctt gct gga gcg tgg tcg cgc cgc gac acc
pro val thr arg his gly leu ser ser leu leu ala gly ala trp ser arg arg asp thr
301/101 331/111
ctc cgc ctg acc gat gcc ctc tac gtc gag ctg gcc gaa acg gca ggt ctg gtg ttg ttg
leu arg leu thr asp ala leu tyr val glu leu ala glu thr ala gly leu val leu leu
361/121 391/131
acc acc gac gaa aga ttg gca cgc gcc tgg ccc tcg gct cac gcc atc ggc tga
thr thr asp glu arg leu ala arg ala trp pro ser ala his ala ile gly)OPA

SEQ ID NOS: 674-675

FIGURE 40D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0549c

1/1 31/11
tga gtt cga agc gtg aga gca tcg ccc act tcg ccg ccg gag cag gtg gtc gtc gac gcg
OPA (val arg ser val arg ala ser pro thr ser pro pro glu gln val val val asp ala
61/21 91/31
agt gcc atg gtg gat cta ctg gct cgc act agc gat ccg tgc tct gcg gtg cgc gcg ccg
ser ala met val asp leu leu ala arg thr ser asp arg cys ser ala val arg ala arg
121/41 151/51
ctg gct ccg acc gcg atg cac gcg ccg gcg cac ttc gat gca gag gtg ttg tcg gcg ctg
leu ala arg thr ala met his ala pro ala his phe asp ala glu val leu ser ala leu
181/61 211/71
ggg cgc atg cag cgc gcc ggc gca ctc acc gtt gcc tat gtc gat gcg gca ctg gag gag
gly arg met gln arg ala gly ala leu thr val ala tyr val asp ala ala leu glu glu
241/81 271/91
ttg cga cag gtg ccg gtg act cga cac ggt ctt tcg tcg ctg ctt gct gga gcg tgg tcg
leu arg gln val pro val thr arg his gly leu ser ser leu leu ala gly ala trp ser
301/101 331/111
cgc cgc gac acc ctc cgc ctg acc gat gcc ctc tac gtc gag ctg gcc gaa acg gca ggt
arg arg asp thr leu arg leu thr asp ala leu tyr val glu leu ala glu thr ala gly
361/121 391/131
ctg gtg ttg ttg acc acc gac gaa aga ttg gca cgc gcc tgg ccc tcg gct cac gcc atc
leu val leu leu thr thr asp glu arg leu ala arg ala trp pro ser ala his ala ile
421/141
ggc tga
gly)OPA

SEQ ID NOS: 676-677

FIGURE 40E

130/185

SEQ ID NO: 678
SEQ ID NO: 679

1/1 31/11
CCT GGC CGG GAC GCC TAC GTG TAG CCC GCG GCT AGC ACA GGA TAG CCA TTG TTG TGC GGT
(pro gly arg asp ala tyr val) AMB (pro ala ala ser thr gly) AMB (pro leu leu cys gly)
61/21 91/31
AGC GCC AAA ACG ATC AGC CCT TCG CGG ACA TGT CAG CAC CCG CCT TGG CCG GGA GAG CGG
ser ala lys thr ile ser pro ser arg thr cys gln his pro pro trp pro gly glu arg
121/41 151/51
CGT CGT GAC CGT GCT GTC ACC ACG TCT GGT TAG GCT CGG GGC GCG GGC TGG CGC GGA GGA
arg arg asp arg ala val thr thr ser gly) AMB (ala arg gly ala gly trp arg gly gly
181/61 211/71
GGT GTG TTG CGG AGG AGG TGT GTT GTA GTG GGG ACG GCG GAT CGG CCG TTG GAC GCC TCG
gly val leu arg arg arg cys val val val gly thr ala asp arg pro leu asp ala ser
241/81 271/91
GCC TTG CGG GAC TGG GCA CAC GCC GTC GTC AGC GAT C
ala leu arg asp trp ala his ala val val ser asp)

SEQ ID NOS: 678-682

FIGURE 41A

SEQ ID NO: 683
SEQ ID NO: 684

1/1 31/11
CTG GCC GGG ACG CCT ACG TGT AGC CCG CGG CTA GCA CAG GAT AGC CAT TGT TGT GCG GTA
(leu ala gly thr pro thr cys ser pro arg leu ala gln asp ser his cys cys ala val
61/21 91/31
GCG CCA AAA CGA TCA GCC CTT CGC GGA CAT GTC AGC ACC CGC CTT GGC CGG GAG AGC GGC
ala pro lys arg ser ala leu arg gly his val ser thr arg leu gly arg glu ser gly
121/41 151/51
GTC GTG ACC GTG CTG TCA CCA CGT CTG GTT AGG CTC GGG GCG CGG GCT GGC GCG GAG GAG
val val thr val leu ser pro arg leu val arg leu gly ala arg ala gly ala glu glu
181/61 211/71
GTG TGT TGC GGA GGA GGT GTG TTG TAG TGG GGA CGG CGG ATC GGC CGT TGG ACG CCT CGG
val cys cys gly gly gly val leu) AMB (trp gly arg arg ile gly arg trp thr pro arg
241/81 271/91
CCT TGC GGG ACT GGG CAC ACG CCG TCG TCA GCG ATC
pro cys gly thr gly his thr pro ser ser ala ile)

SEQ ID NOS: 683-685

FIGURE 41B

131/185

SEQ ID NO: 686
SEQ ID NO: 687
SEQ ID NO: 689

```

1/1                               31/11
TGG CCG GGA CGC CTA CGT GTA GCC CGC GGC TAG CAC AGG ATA GCC ATT GTT GTG CGG TAG
(trp pro gly arg leu arg val ala arg gly) AMB (his arg ile ala ile val val arg) AMB
61/21                               91/31  SEQ ID NO: 689
CGC CAA AAC GAT CAG CCC TTC GCG GAC ATG TCA GCA CCC GCC TTG GCC GGG AGA GCG GCG
arg gln asn asp gln pro phe ala asp met ser ala pro ala leu ala gly arg ala ala
121/41                               151/51
TCG TGA CCG TGC TGT CAC CAC GTC TGG TTA GGC TCG GGG CGC GGG CTG GCG CGG AGG AGG
ser) OPA (pro cys cys his his val trp leu gly ser gly arg gly leu ala arg arg arg
181/61  SEQ ID NO: 690                               211/71
TGT GTT GCG GAG GAG GTG TGT TGT AGT GGG GAC GGC GGA TCG GCC GTT GGA CGC CTC GGC
cys val ala glu glu val cys cys ser gly asp gly gly ser ala val gly arg leu gly
241/81                               271/91
CTT GCG GGA CTG GGC ACA CGC CGT CGT CAG CGA TC
leu ala gly leu gly thr arg arg arg gln arg)

```

SEQ ID NOS: 686-690

FIGURE 41C

Coding sequence Rv2975c predicted by Cole et al, 1998 (Nature 393: 537-544) and containing seq41A

```

1/1                               31/11
gtg ggg acg gcg gat cgg ccg ttg gac gcc tcg gcc ttg cgg gac tgg gca cac gcc gtc
val gly thr ala asp arg pro leu asp ala ser ala leu arg asp trp ala his ala val
61/21                               91/31
gtc agc gat ctg atc ctc cac atc gac gag atc aac cgg ctc aat gtg ttc ccg gtc gct
val ser asp leu ile leu his ile asp glu ile asn arg leu asn val phe pro val ala
121/41                               151/51
gac tcc gat acc ggc gtc aac atg ctg ttc acc atg cgt gcc gcg gtc gta gaa gct gat
asp ser asp thr gly val asn met leu phe thr met arg ala ala val val glu ala asp
181/61                               211/71
ttg cac gcg aat tcg cag gct gac gcc gaa gac gtg gcg cgg gtt gcg gcc gct ctc gcg
leu his ala asn ser gln ala asp ala glu asp val ala arg val ala ala ala leu ala
241/81
gcc ggc gcg cgt tga
ala gly ala arg) OPA

```

SEQ ID NO: 691
SEQ ID NO: 692

SEQ ID NOS: 691-692

FIGURE 41D

132/185

ORF according to Cole et al, 1998 (Nature 393: 537-544) and containing Rv2975c

1/1 31/11
tag gct cgg ggc gcg ggc tgg cgc gga gga ggt gtg ttg cgg agg agg tgt gtt gta gtg
AMB (ala arg gly ala gly trp arg gly gly gly val leu arg arg arg cys val val val
61/21 SEQ ID NO: 694 91/31
ggg acg gcg gat cgg ccg ttg gac gcc tcg gcc ttg cgg gac tgg gca cac gcc gtc gtc
gly thr ala asp arg pro leu asp ala ser ala leu arg asp trp ala his ala val val
121/41 151/51
agc gat ctg atc ctc cac atc gac gag atc aac cgg ctc aat gtg ttc ccg gtc gct gac
ser asp leu ile leu his ile asp glu ile asn arg leu asn val phe pro val ala asp
181/61 211/71
tcc gat acc ggc gtc aac atg ctg ttc acc atg cgt gcc gcg gtc gta gaa gct gat ttg
ser asp thr gly val asn met leu phe thr met arg ala ala val val glu ala asp leu
241/81 271/91
cac gcg aat tcg cag gct gac gcc gaa gac gtg gcg cgg gtt gcg gcc gct ctc gcg gcc
his ala asn ser gln ala asp ala glu asp val ala arg val ala ala ala leu ala ala
301/101
ggc gcg cgt tga
gly ala arg) OPA

SEQ ID NOS: 693-694

FIGURE 41E

sequence Rv 2974C predicted by Cole et al. (Nature 393:537-544) and which may be in the same reading frame as Seq41D. The sequencing of this region reveals, in one case out of three, a deletion of two nucleotides

1/1 31/11
ttg aac gga gct cgc ggc aac tcc ggc gtg atc ctg tcc cag atc ctg cgc ggg atc gca
(leu asn gly ala arg gly asn ser gly val ile leu ser gln ile leu arg gly ile ala
61/21 91/31
gag gtg acc gcg act gcg gcc gcc gcc tct ggc gcg gta ttg cgg gcg gtc gac gcc aac
glu val thr ala thr ala ala ala ala ser gly ala val leu arg ala val asp ala asn
121/41 151/51
gcc ctc ggg gcc gcg ttg tgg cgc ggc gtc gag ttg gtc gtc gcg tcg atg ggt ggc gtg
ala leu gly ala ala leu trp arg gly val glu leu val val ala ser met gly gly val
181/61 211/71
gag gtg ccg gga act atc gtc tcg gtg ctg cgg gcc gcc gcc gga gcc gtc gac cag tgc
glu val pro gly thr ile val ser val leu arg ala ala ala gly ala val asp gln cys
241/81 271/91
gag gag ggg ttg gcc ggt gcg gtc acc gcc gcc ggt gac gcg gcg gtc atc gcg ctg
ala his glu gly leu ala gly ala val thr ala ala gly asp ala ala val ile ala leu
301/101 331/111
gaa aag acc ccc gaa cag ctt gac gtg ctc gcc gat gcg ggc gcg gtg gac gcc ggc gga
glu lys thr pro glu gln leu asp val leu ala asp ala gly ala val asp ala gly gly

SEQ ID NOS: 695-696

FIGURE 41F

133/185

361/121	391/131
cgg ggc ctg ctg gtt ctg ctg gac gcg ttg	cgc tcc acc atc tgc ggg cag gca cct gcc
arg gly leu leu val leu leu asp ala leu	arg ser thr ile cys gly gln ala pro ala
421/141	451/151
cgg gcg gtc tac gaa ccc tcg ccg cgc gcg	ttg ccg acc gac acg gct acc caa cgc ccc
arg ala val tyr glu pro ser pro arg ala	leu pro thr asp thr ala thr gln arg pro
481/161	511/171
gcc ccg caa ttc gag gtg atg tat ctg ttg	gcg gta tgt gat gct gca gcg gcg gac cag
ala pro gln phe glu val met tyr leu leu	ala val cys asp ala ala ala ala asp gln
541/181	571/191
ttg ccg gat cga ctc aag gaa ttg ggt gag	tcg gtg gcc atc gcc gct gct ccg ccc gac
leu arg asp arg leu lys glu leu gly glu	ser val ala ile ala ala ala pro pro asp
601/201	631/211
agc tac tcc gta cac gtc cac acc gac gac	gcc ggt gcc gcc gtg gaa gcc gga ttg gcg
ser tyr ser val his val his thr asp asp	ala gly ala ala val glu ala gly leu ala
661/221	691/231
gtg ggg cga gtt agc ccg atc gtg atc tcg	gcg ctc ggt tcc ggg acc agc gga ttg ccg
val gly arg val ser arg ile val ile ser	ala leu gly ser gly thr ser gly leu pro
721/241	751/251
gcc ggt ggc tgg acg ccg ggc cgc gcc gtg	ctg gcg gtc gtc gac ggc gac ggt gcc gcc
ala gly gly trp thr arg gly arg ala val	leu ala val val asp gly asp gly ala ala
781/261	811/271
gag ctg ttc gcc ggg gag ggc gcc tgc gtg	ctg cga ccg ggt cca gac gcc gtg aca ccg
glu leu phe ala gly glu gly ala cys val	leu arg pro gly pro asp ala val thr pro
841/281	871/291
gcc gcc gat atc agt gcc cac cag ctg gtg	ccg gcc gtg gta gac acc ggc gcc gcg cac
ala ala asp ile ser ala his gln leu val	arg ala val val asp thr gly ala ala his
901/301	931/311
gtg atg gtg ctg ccc aat ggc tat gtg gcc	gcc gaa gaa ctg gtg gcc ggg tgt acc gcg
val met val leu pro asn gly tyr val ala	ala glu glu leu val ala gly cys thr ala
961/321	991/331
gcg atc ggc tgg ggc gtc gac gtg gta ccc	gtg ccg acc gga tcg atg gtg cag ggg ttg
ala ile gly trp gly val asp val val pro	val pro thr gly ser met val gln gly leu
1021/341	1051/351
gcc gcg ctg gcc gtg cat gac gcg gcc cgc	cag gcc gtc gac gac ggc tac agc atg gcc
ala ala leu ala val his asp ala ala arg	gln ala val asp asp gly tyr ser met ala
1081/361	1111/371
cgt gcc gcc ggt gct tcc ccg cac gga tcg	gtg cgc att gcc acc caa aag gcg ctg acc
arg ala ala gly ala ser arg his gly ser	val arg ile ala thr gln lys ala leu thr
1141/381	1171/391
tgg gcc ggt acc tgc aag ccg ggc gac ggt	ctg ggt atc gcg ggc gac gag gtg ctg atc
trp ala gly thr cys lys pro gly asp gly	leu gly ile ala gly asp glu val leu ile
1201/401	1231/411
gtc gcc gac gat gtc gcc gcg gcg gcc atc	ggt ctg gtc gac ctg ttg ttg gca tcg gga
val ala asp asp val ala ala ala ala ile	gly leu val asp leu leu leu ala ser gly
1261/421	1291/431
ggc gat ctg gtg acg gtg cta att ggc gcc	ggc gta acc gaa gac gtg gct gtc gtc ctg
gly asp leu val thr val leu ile gly ala	gly val thr glu asp val ala val val leu
1321/441	1351/451
gaa ccg cat gtg cac gac cac cat cca ggc	acc gag ctg gtc tcc tac cgc acc gga cac
glu arg his val his asp his his pro gly	thr glu leu val ser tyr arg thr gly his
1381/461	1411/471
cgc ggc gac gcg ctg ctg atc ggg gtc gag tag	
arg gly asp ala leu leu ile gly val glu	AMB

SEQ ID NDS: 695-696

FIGURE 41F (continued)

Seq41T comprising seq 41F and seq 41S

1/1 **SEQ ID NO: 702** **SEQ ID NO: 717** 31/11
 tta ggc tgc ggg cgc ggg ctg gcg cgg agg agg tgt gtt gcg gag gag gtg tgt tgt agt
 leu gly ser gly arg gly leu ala arg arg arg cys val ala glu glu val cys cys ser
 AMB(ala arg gly ala gly trp arg gly gly gly val leu arg arg arg cys val val val
 (arg leu gly ala arg ala gly ala glu glu val cys cys gly gly gly val leu) AMB(trp
 61/21 91/31 **SEQ ID NO: 719**
 ggg gac ggc gga tgc gcc gtt gga cgc ctc gcc ctt gcg gga ctg gcc aca cgc cgt cgt
 gly asp gly gly ser ala val gly arg leu gly leu ala gly leu thr arg arg arg
 gly thr ala asp arg pro leu asp ala ser ala leu arg asp trp ala his ala val val
 gly arg arg ile gly arg trp thr pro arg pro cys gly thr gly his thr pro ser ser
 121/41 151/51
 cag cga tct gat cct cca cat cga cga gat caa ccg gct caa tgt gtt ccc ggt cgc tga
 gln arg ser asp pro pro his arg arg asp gln pro ala gln cys val pro gly arg) OPA
 ser asp leu ile leu his ile asp glu ile asn arg leu asn val phe pro val ala asp
 ala ile) OPA (ser ser thr ser thr arg ser thr gly ser met cys ser arg ser leu thr
 181/61 **SEQ ID NO: 720** 211/71
 ctc cga tac cgg cgt caa cat gct gtt cac cat gcg tgc cgc ggt cgt aga agc tga ttt
 (leu arg tyr arg arg gln his ala val his ala cys arg gly arg arg ser) OPA (phe
 ser asp thr gly val asn met leu phe thr met arg ala ala val val glu ala asp leu
 pro ile pro ala ser thr cys cys ser pro cys val pro arg ser) AMB(lys leu ile cys
 241/81 271/91 **SEQ ID NO: 721**
 gca cgc gaa ttc gca ggc tga cgc cga aga cgt gcc gcg ggt tgc gcc cgc tct cgc gcc
 ala arg glu phe ala gly) OPA (arg arg arg arg gly ala gly cys gly arg ser arg gly
 his ala asn ser gln ala asp ala glu asp val ala arg val ala ala leu ala ala
 thr arg ile arg arg leu thr pro lys thr trp arg gly leu arg pro leu ser arg pro
 301/101 **SEQ ID NO: 701** 331/111
 cgg cgc gcg ttg aac gga gct cgc gcc aac tcc gcc gtg atc ctg tcc cag atc ctg cgc
 arg arg ala leu asn gly ala arg gly asn ser gly val ile leu ser gln ile leu arg
 gly ala arg) OPA (thr glu leu ala ala thr pro ala) OPA (ser cys pro arg ser cys ala
 ala arg val glu arg ser ser arg gln leu arg arg asp pro val pro asp pro ala arg
 361/121 **SEQ ID NO: 704** 391/131 **SEQ ID NO: 705**
 ggg atc gca gag gtg acc gcg act gcg gcc gcc gcc tct gcc gcg gta ttg cgg gcg gtc
 gly ile ala glu val thr ala thr ala ala ala ser gly ala val leu arg ala val
 gly ser gln arg) OPA (pro arg leu arg pro pro pro leu ala arg tyr cys gly arg ser
 asp arg arg gly asp arg asp cys gly arg arg leu trp arg gly ile ala gly gly arg
 421/141 **SEQ ID NO: 706** 451/151
 gac gcc aac gcc ctc ggg gcc gcg ttg tgg cgc gcc gtc gag ttg gtc gtc gcg tgc atg
 asp ala asn ala leu gly ala ala leu trp arg gly val glu leu val val ala ser met
 thr pro thr pro ser gly pro arg cys gly ala ala ser ser trp ser ser arg arg trp
 arg gln arg pro arg gly arg val val ala arg arg arg val gly arg arg val asp gly
 481/161 511/171
 ggt gcc gtg gag gtg ccg gga act atc gtc tgc gtg ctg cgg gcc gcc gcc gga gcc gtc
 gly gly val glu val pro gly thr ile val ser val leu arg ala ala gly ala val
 val ala trp arg cys arg glu leu ser ser arg cys cys gly pro pro pro glu pro ser
 trp arg gly gly ala gly asn tyr arg leu gly ala ala gly arg arg arg ser arg arg
 541/181 571/191
 gac cag tgc gcg cac gag ggg ttg gcc ggt gcg gtc acc gcc gcc ggt gac gcg gcg gtc
 asp gln cys ala his glu gly leu ala gly ala val thr ala ala gly asp ala ala val
 thr ser ala arg thr arg gly trp pro val arg ser pro pro pro val thr arg arg ser
 pro val arg ala arg gly val gly arg cys gly his arg arg arg) OPA (arg gly gly his
 601/201 631/211 **SEQ ID NO: 722**
 atc gcg ctg gaa aag acc ccc gaa cag ctt gac gtg ctc gcc gat gcg gcc gcg gtg gac
 ile ala leu glu lys thr pro glu gln leu asp val leu ala asp ala gly ala val asp
 ser arg trp lys arg pro pro asn ser leu thr cys ser pro met arg ala arg trp thr
 arg ala gly lys asp pro arg thr ala) OPA (arg ala arg arg cys gly arg gly gly arg
 661/221 691/231 **SEQ ID NO: 723**
 gcc gcc gga cgg gcc ctg ctg gtt ctg ctg gac gcg ttg cgc tcc acc atc tgc ggg cag
 ala gly gly arg gly leu leu val leu leu asp ala leu arg ser thr ile cys gly gln
 pro ala asp gly ala cys trp phe cys trp thr arg cys ala pro pro ser ala gly arg
 arg arg thr gly pro ala gly ser ala gly arg val ala leu his his l u arg ala gly

SEQ ID NOS: 697-727

FIGURE 41G

721/241

gca cct gcc cgg gcg gtc tac gaa ccc tcg ccg cgc gcg ttg ccg acc gac acg gct acc
ala pro ala arg ala val tyr glu pro ser pro arg ala leu pro thr asp thr ala thr
his leu pro gly arg ser thr asn pro arg arg ala arg cys arg pro thr arg leu pro
thr cys pro gly gly leu arg thr leu ala ala arg val ala asp arg his gly tyr pro

781/261

caa cgc ccc gcc ccg caa ttc gag gtg atg tat ctg ttg gcg gta tgt gat gct gca gcg
gln arg pro ala pro gln phe glu val met tyr leu leu ala val cys asp ala ala ala
asn ala pro pro arg asn ser arg) OPA (cys ile cys trp arg tyr val met leu gln arg
thr pro arg pro ala ile arg gly asp val ser val gly gly met) OPA cys cys ser gly

841/281

gcg gac cag ttg ccg gat cga ctc aag gaa ttg ggt gag tcg gtg gcc atc gcc gct gct
ala asp gln leu arg asp arg leu lys glu leu gly glu ser val ala ile ala ala ala
arg thr ser cys gly ile asp ser arg asn trp val ser arg trp pro ser pro leu leu
gly pro val ala gly ser thr gln gly ile gly) OPA (val gly gly his arg arg cys ser

901/301

ccg ccc gac agc tac tcc gta cac gtc cac acc gac gac gcc ggt gcc gcc gtc gaa gcc
pro pro asp ser tyr ser val his val his thr asp asp ala gly ala ala val glu ala
arg pro thr ala thr pro tyr thr ser thr pro thr thr pro val pro pro trp lys pro
ala arg gln leu leu arg thr arg pro his arg arg arg arg cys arg arg gly ser arg

961/321

gga ttg gcg gtg ggg cga gtt agc cgg atc gtg atc tcg gcg ctc ggt tcc ggg acc agc
gly leu ala val gly arg val ser arg ile val ile ser ala leu gly ser gly thr ser
asp trp arg trp gly glu leu ala gly ser) OPA (ser arg arg ser val pro gly pro ala.
ile gly gly gly ala ser) AMB (pro asp arg asp leu gly ala arg phe arg asp gln arg

1021/341

gga ttg ccg gcc ggt gcc tgg acg cgg gcc cgc gcc gtg ctg gcg gtc gac gcc gac
gly leu pro ala gly gly trp thr arg gly arg ala val leu ala val val asp gly asp
asp cys arg pro val ala gly arg gly ala ala pro cys trp arg ser ser thr ala thr
ile ala gly arg trp leu asp ala gly pro arg arg ala gly gly arg arg arg arg arg

1081/361

ggt gcc gcc gag ctg ttc gcc ggg gag gcc gcc tgc gtg ctg cga ccg ggt cca gac gcc
gly ala ala glu leu phe ala gly glu gly ala cys val leu arg pro gly pro asp ala
val pro pro ser cys ser pro gly arg ala pro ala cys cys asp arg val gln thr pro)
cys arg arg ala val arg arg gly gly arg leu arg ala ala thr gly ser arg arg arg

1141/381

gtg aca ccg gcc gcc gat atc agt gcc cac cag ctg gtg ccg gcc gtg gta gac acc gcc
val thr pro ala ala asp ile ser ala his gln leu val arg ala val val asp (thr gly
OPA (his arg pro pro ile ser val pro thr ser trp cys gly pro trp) AMB thr pro ala
asp thr gly arg arg tyr gln cys pro pro ala gly ala gly arg gly arg his arg arg

1201/401

gcc gcg cac gtg atg gtg ctg ccc aat gcc tat gtg gcc gcc gaa gaa ctg gtg gcc ggg
ala ala his val met val leupro asn gly tyr val ala ala glu glu leu val ala gly
pro arg thr) OPA (trp cys cys pro met ala met trp pro pro lys asn trp trp pro gly
arg ala arg asp gly ala ala gln trp leu cys gly arg arg arg thr gly gly arg val

1261/421

tgt acc gcg gcg atc gcc tgg gcc gtc gac gtg gta ccc gtg ccg acc gga tcg atg gtg
cys thr ala ala ile gly trp gly val asp val pro val pro thr gly ser met val
val pro arg arg ser ala gly ala ser thr trp tyr pro cys arg pro asp arg trp cys
tyr arg gly asp arg leu gly arg arg arg gly thr arg ala asp arg ile asp gly ala

1321/441

cag ggg ttg gcc gcg ctg gcc gtg cat gac gcg gcc cgc cag gcc gtc gac gac gcc tac
gln gly leu ala ala leu ala val his asp ala ala arg gln ala val asp asp gly tyr
arg gly trp pro arg trp pro cys met thr arg pro ala arg pro ser thr thr ala thr
gly val gly arg ala gly arg ala) OPA (arg gly pro pro gly arg arg arg arg leu gln

1381/461

agc atg gcc cgt gcc gcc ggt gct tcc ccg cac gga tcg gtg cgc att gcc acc caa aag
ser met ala arg ala ala gly ala ser arg his gly ser val arg ile ala thr gln lys
ala trp pro val pro pro val leu pro gly thr asp arg cys ala leu pro pro lys arg
his gly pro cys arg arg cys phe pro ala arg ile gly ala his cys his pro lys gly

SEQ ID : NOS: 697-727

FIGURE 41G (continued 1)

1441/481
gcg ctg acc tgg gcc ggt acc tgc aag ccg ggc gac ggt ctg ggt atc gcg ggc gac gag
ala leu thr trp ala gly thr cys lys pro gly asp gly leu gly ile ala gly asp glu
arg) OPA (pro gly pro val pro ala ser arg ala thr val trp val ser arg ala thr arg
ala asp leu gly arg tyr leu gln ala gly arg arg ser gly tyr arg gly arg arg gly
1501/501 **SEQ ID NO: 712**
gtg ctg atc gtc gcc gac gat gtc gcc gcg ggc gcc atc ggt ctg gtc gac ctg ttg ttg
val leu ile val ala asp asp val ala ala ala ile gly leu val asp leu leu leu
cys) OPA (ser ser pro thr met ser pro arg arg pro ser val trp ser thr cys cys trp
ala asp arg arg arg cys arg arg gly gly his arg ser gly arg pro val val gly
1561/521 **SEQ ID NO: 713**
gca tgc gga ggc gat ctg gtg acg gtg cta att ggc gcc gta acc gaa gac gtg gct
ala ser gly gly asp leu val thr val leu ile gly ala gly val thr glu asp val ala
his arg glu ala ile trp) OPA arg cys OCH (leu ala pro ala) OCH (pro lys thr trp leu
ile gly arg arg ser gly asp gly ala asn trp arg arg arg asn arg arg arg gly cys
1621/541 **SEQ ID NO: 714** 1651/551 **SEQ ID NO: 715**
gtc gtc ctg gaa cgg cat gtg cac gac cac cat cca ggc acc gag ctg gtc tcc tac ccg
val val leu glu arg his val his asp his his pro gly thr glu leu val ser tyr arg
ser ser trp asn gly met cys thr thr thr ile gln ala pro ser trp ser pro thr ala
arg pro gly thr ala cys ala arg pro pro ser arg his arg ala gly leu leu pro his
1681/561 1711/571
acc gga cac cgc ggc gac gcg ctg ctg atc ggg gtc gag tag
thr gly his arg gly asp ala leu leu ile gly val glu) AMB
pro asp thr ala thr arg cys) OPA (ser gly ser) ser
arg thr pro arg arg arg ala ala asp arg gly arg val
SEQ ID NO: 716

SEQ ID NOS: 697-727 (continued 2)

FIGURE 41G (continued 2)

SEQ ID NO: 728 1/1
GCC GGT AAC GCC GCG TCC CAG TGC TAT CCG TCC GCC GGA CCG CCC GAA ACA TCA GCG GCG
SEQ ID NO: 729 ala gly asn ala ala ser gln cys tyr pro ser ala gly pro pro glu thr ser ala ala
61/21 91/31
GGC GCC CCG GTC GGC CGC GGC CGG GCT CGA CCC GCT CCA CCT GGC CAT CAG CGA CCA GGT
gly ala pro val gly arg gly arg ala arg pro ala pro pro gly his gln arg pro gly
121/41 151/51
TAT CGA GGT GGA AGC GGA CGG TGT TGG GAT GCA CGC CCA ACT TGC CGG CGA TCG CGG CGA
tyr arg gly gly ser gly arg cys trp asp ala arg pro thr cys arg arg ser arg arg
181/61 211/71
TGC TCA TCG GAA CCC GCG ACG CAC ACA ATG CCC GCA GCA CCG CAC GAC GGC GCC CCA CCG
cys ser ser glu pro ala thr his thr met pro ala ala pro his asp gly ala pro pro
241/81 271/91
GCT CTT GCA GTG ACC TGA TGA TGA CAC TCA CCC CCA TAA GGC TCG TCG GCT GCG CCT GAG
ala leu ala val thr) OPA OPA OPA (his ser pro pro) OCH (gly ser ser ala ala pro glu
301/101 **SEQ ID NO: 730** 331/111 **SEQ ID NO: 731**
CAA TGC AGT AAG TTT ACA CAA ACG GAC TTG TAA AAA CCT GCG GAG GTG GGG TCT ATG GCC
gln cys ser lys phe thr gln thr asp leu) OCH (lys pro ala glu val gly ser met ala
361/121 391/131 **SEQ ID NO: 732**
AAC AAA CGT GGC AAT GCC GGG CAG CCT CTG CCC TTG TCG GAT C
asn lys arg gly asn ala gly gln pro leu pro leu ser asp)

SEQ ID NOS: 728-732

FIGURE 42A

137/185

SEQ ID NO: 733

1
1/1
CCG GTA ACG CCG CGT CCC AGT GCT ATC CGT CCG CCG GAC CGC CCG AAA CAT CAG CGG CGG
pro val thr pro arg pro ser ala ile arg pro pro asp arg pro lys his gln arg arg
61/21 → SEQ ID NO: 734
GCG CCC CCG TCG GCC GCG GCC GGG CTC GAC CCG CTC CAC CTG GCC ATC AGC GAC CAG GTT
ala pro arg ser ala ala ala gly leu asp pro leu his leu ala ile ser asp gln val
121/41
ATC GAG GTG GAA GCG GAC GGT GTT GGG ATG CAC GCC CAA CTT GCC GGC GAT CGC GGC GAT
ile glu val glu ala asp gly val gly met his ala gln leu ala gly asp arg gly asp
181/61
GCT CAT CGG AAC CCG CGA CGC ACA CAA TGC CCG CAG CAC CGC ACG ACG GCG CCC CAC CGG
ala his arg asn pro arg arg thr gln cys pro gln his arg thr thr ala pro his arg
241/81
CTC TTG CAG TGA CCT GAT GAT GAC ACT CAC CCC CAT AAG GCT CGT CCG CTG CGC CTG AGC
leu leu gln) OPA (pro asp asp asp thr his pro his lys ala arg arg leu arg leu ser
301/101
AAT GCA GTA AGT TTA CAC AAA CGG ACT TGT AAA AAC CTG CCG AGG TGG GGT CTA TGG CCA
asn ala val ser leu his lys arg thr cys lys asn leu arg arg trp gly leu trp pro
361/121
ACA AAC GTG GCA ATG CCG GGC AGC CTC TGC CCT TGT CGG ATC
thr asn val ala met pro gly ser leu cys pro cys arg ile)

SEQ ID NOS: 733-735

FIGURE 42B

SEQ ID NO: 736

1/1
CGG TAA CGC CGC GTC CCA GTG CTA TCC GTC CGC CGG ACC GCC CGA AAC ATC AGC GGC GGG
arg OCH (arg arg val pro val leu ser val arg arg thr ala arg asn ile ser gly gly
61/21 → SEQ ID NO: 737
CGC CCC GGT CGG CCG CGG CCG GGC TCG ACC CGC TCC ACC TGG CCA TCA GCG ACC AGG TTA
arg pro gly arg pro arg pro gly ser thr arg ser thr trp pro ser ala thr arg leu
121/41
TCG AGG TGG AAG CGG ACG GTG TTG GGA TGC ACG CCC AAC TTG CCG GCG ATC GCG GCG ATG
ser arg trp lys arg thr val leu gly cys thr pro asn leu pro ala ile ala ala met
181/61
CTC ATC GGA ACC CGC GAC GCA CAC AAT GCC CGC AGC ACC GCA CGA CGG CGC CCC ACC GGC
leu ile gly thr arg asp ala his asn ala arg ser thr ala arg arg arg pro thr gly
241/81
TCT TGC AGT GAC CTG ATG ATG ACA CTC ACC CCC ATA AGG CTC GTC GGC TGC GCC TGA GCA
ser cys ser asp leu met met thr leu thr pro ile arg leu val gly cys ala) OPA ala
301/101
ATG CAG TAA GTT TAC ACA AAC GGA CTT GTA AAA ACC TGC GGA GGT GGG GTC TAT GGC CAA
met gln OCH (val tyr thr asn gly leu val lys thr cys gly gly gly val tyr gly gln
361/121
CAA ACG TGG CAA TGC CGG GCA GCC TCT GCC CTT GTC GGA TC
gln thr trp gln cys arg ala ala ser ala leu val gly)

SEQ ID NOS: 736-738

FIGURE 42C

Coding sequence Rv2622 predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq42A:

1/1 31/11
 atg gcc aac aaa cgt ggc aat gcc ggg cag cct ctg ccc ttg tcg gat cga gac gac gac
 Met ala asn lys arg gly asn ala gly gln pro leu pro leu ser asp arg asp asp asp
 61/21 → SEQ ID NO: 740 91/31
 cac atg cag ggg cac tgg ctg ctg gcc cgg ctg ggc aag cgg gtg ctg cgt ccc ggc ggc
 his met gln gly his trp leu leu ala arg leu gly lys arg val leu arg pro gly gly
 121/41 151/51
 gtc gaa ctc acc cgg aca ctg ctg gcc cgc gcc gag gtg acc gac gcc gac gtg ctc gag
 val glu leu thr arg thr leu leu ala arg ala glu val thr asp ala asp val leu glu
 181/61 211/71
 ctg gca ccg ggc ctg ggc cgc acc gca gcc gaa atc ttg gcc cgc aac ccg cgg tcg tac
 leu ala pro gly leu gly arg thr ala ala glu ile leu ala arg asn pro arg ser tyr
 241/81 271/91
 gtg ggg gcg gag agc gat ccc aac gcg gcc aac ctg gtc cga cac gtt ctc gcc ggc cgc
 val gly ala glu ser asp pro asn ala ala asn leu val arg his val leu ala gly arg
 301/101 331/111
 ggc gac gtc cgg gtc acc gac gcg gcc gat acc gga tta tcc gac gcc agc gcc gat gtc
 gly asp val arg val thr asp ala ala asp thr gly leu ser asp ala ser ala asp val
 361/121 391/131
 gtc atc ggc gag gcg atg ctg acc atg caa ggc aac gcg gct aaa cac acg atc gtc gcc
 val ile gly glu ala met leu thr met gln gly asn ala ala lys his thr ile val ala
 421/141 451/151
 gag gcg gcg cgg gtg ctg agg ccg ggt ggc cgc tac gcg att cac gaa cta gcg ctg gtg
 glu ala ala arg val leu arg pro gly gly arg tyr ala ile his glu leu ala leu val
 481/161 511/171
 ccg gac gac gtc gca gag cag gtc cgc acc gac ctg cgg cag tcg ctg gcc cgc gcg ctc
 pro asp asp val ala glu gln val arg thr asp leu arg gln ser leu ala arg ala leu
 541/181 571/191
 aag gtc aat gcg cgt ccg ctg acc gtt gcg gaa tgg tcg cac ctc tta gcg ggc cat gga
 lys val asn ala arg pro leu thr val ala glu trp ser his leu leu ala gly his gly
 601/201 631/211
 ctg gtc gtc gaa cac gtt gtc acc gct tcc atg gcg ttg tta caa ccg cga cgg gtg atc
 leu val val glu his val val thr ala ser met ala leu leu gln pro arg arg val ile
 661/221 691/231
 gct gac gaa ggc ctc ctg ggt gcg ctg cgg ttc gcc gga aac ctg ctc atc cat cgt gcc
 ala asp glu gly leu leu gly ala leu arg phe ala gly asn leu leu ile his arg ala
 721/241 751/251
 gcg cgt cgg cga gtc ctg ttg atg cgc cac aca ttc cgc agg cat cgt gaa cgc ttg aca
 ala arg arg arg val leu leu met arg his thr phe arg arg his arg glu arg leu thr
 781/261 811/271
 gcc gtc gcc att gtc gcg cac aaa ccg cac gtc gat tcg tga
 ala val ala ile val ala his lys pro his val asp ser) OPA

SEQ ID NOS: 739-740

FIGURE 42D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv2622

1/1 31/11
 taa aaa cct gcg gag gtg ggg tct atg gcc aac aaa cgt ggc aat gcc ggg cag cct ctg
 OCH(lys pro ala glu val gly ser met ala asn lys arg gly asn ala gly gln pro leu
 61/21 ~~SEQ ID NO: 741~~ 91/31
 ccc ttg tcg gat cga gac gac gac cac atg cag ggg cac tgg ctg ctg gcc cgg ctg ggc
 pro leu ser asp arg asp asp asp his met gln gly his trp leu leu ala arg leu gly
 121/41 151/51
 aag cgg gtg ctg cgt ccc ggc ggc gtc gaa ctc acc cgg aca ctg ctg gcc cgc gcc gag
 lys arg val leu arg pro gly gly val glu leu thr arg thr leu leu ala arg ala glu
 181/61 211/71
 gtg acc gac gcc gac gtg ctc gag ctg gca ccg ggc ctg ggc cgc acc gca gcc gaa atc
 val thr asp ala asp val leu glu leu ala pro gly leu gly arg thr ala ala glu ile
 241/81 271/91
 ttg gcc cgc aac ccg cgg tcg tac gtg ggg gcg gag agc gat ccc aac gcg gcc aac ctg
 leu ala arg asn pro arg ser tyr val gly ala glu ser asp pro asn ala ala asn leu
 301/101 331/111
 gtc cga cac gtt ctc gcc ggc cgc ggc gac gtc cgg gtc acc gac gcg gcc gat acc gga
 val arg his val leu ala gly arg gly asp val arg val thr asp ala ala asp thr gly
 361/121 391/131
 tta tcc gac gcc agc gcc gat gtc gtc atc ggc gag gcg atg ctg acc atg caa ggc aac
 leu ser asp ala ser ala asp val val ile gly glu ala met leu thr met gln gly asn
 421/141 451/151
 gcg gct aaa cac acg atc gtc gcc gag gcg gcg cgg gtg ctg agg ccg ggt ggc cgc tac
 ala ala lys his thr ile val ala glu ala ala arg val leu arg pro gly gly arg tyr
 481/161 511/171
 gcg att cac gaa cta gcg ctg gtg ccg gac gac gtc gca gag cag gtc cgc acc gac ctg
 ala ile his glu leu ala leu val pro asp asp val ala glu gln val arg thr asp leu
 541/181 571/191
 cgg cag tcg ctg gcc cgc gcg ctc aag gtc aat gcg cgt ccg ctg acc gtt gcg gaa tgg
 arg gln ser leu ala arg ala leu lys val asn ala arg pro leu thr val ala glu trp
 601/201 631/211
 tcg cac ctc tta gcg ggc cat gga ctg gtc gtc gaa cac gtt gtc acc gct tcc atg gcg
 ser his leu leu ala gly his gly leu val val glu his val val thr ala ser met ala
 661/221 691/231
 ttg tta caa ccg cga cgg gtg atc gct gac gaa ggc ctc ctg ggt gcg ctg cgg ttc gcc
 leu leu gln pro arg arg val ile ala asp glu gly leu leu gly ala leu arg phe ala
 721/241 751/251
 gga aac ctg ctc atc cat cgt gcc gcg cgt cgg cga gtc ctg ttg atg cgc cac aca ttc
 gly asn leu leu ile his arg ala ala arg arg arg val leu leu met arg his thr phe
 781/261 811/271
 cgc agg cat cgt gaa cgc ttg aca gcc gtc gcc att gtc gcg cac aaa ccg cac gtc gat
 arg arg his arg glu arg leu thr ala val ala ile val ala his lys pro his val asp
 841/281
 tcg tga
 ser)OPA

SEQ ID NOS: 741-742

FIGURE 42E

140/185

1/1 31/11
 SEQ ID NO: 743 atc gcg cgt gac atc gat gac cag ggt cgg ctg tgt ctg gac gtc ggc ggt cga acg gta
 SEQ ID NO: 744 (ile ala arg asp ile asp asp gln gly arg leu cys leu asp val gly gly arg thr val
 61/21 91/31
 gtt gtt tca gcg ggc gac gtg gtg cat ttg cgt taa ctc gcg cgg agc tgg cgt ccc caa
 val val ser ala gly asp val val his leu arg) OCH (leu ala arg ser trp arg pro gln
 121/41 151/51 SEQ ID NO: 745
 aag att aag gtc gcg ggc atg agc tat ccg gag aat gtc ctg gcc gct ggc gag cag gtc
 lys ile lys val ala gly met ser tyr pro glu asn val leu ala ala gly glu gln val
 181/61 211/71
 gtt ctg cac cgc cat ccg cac tgg aat cgc tta atc tgg ccc gtc gtg gtg ctg gtc ttg
 val leu his arg his pro his trp asn arg leu ile trp pro val val val leu val leu
 241/81 271/91
 ctg acc ggg ttg gcg gcg ttc ggg tcc gga ttc gtc aac tcg aca cct tgg cag cag atc
 leu thr gly leu ala ala phe gly ser gly phe val asn ser thr pro trp gln gln ile)

SEQ ID Nds: 743-745

FIGURE 43A

1/1 31/11
 SEQ ID NO: 746 tgc cgc gtg aca tcg atg acc agg gtc ggc tgt gtc tgg acg tcg gcg gtc gaa cgg tag
 (ser arg val thr ser met thr arg val gly cys val trp thr ser ala val glu arg) AMB
 61/21 SEQ ID NO: 747 91/31
 ttg ttt cag cgg gcg acg tgg tgc att tgc gtt aac tcg cgc gga gct ggc gtc ccc aaa
 (leu phe gln arg ala thr trp cys ile cys val asn ser arg gly ala gly val pro lys
 121/41 151/51
 aga tta agg tcg cgg gca tga gct atc ccg aga atg tcc tgg ccg ctg gcg agc agg tcg
 arg leu arg ser arg ala) OPA (ala ile arg arg met ser trp pro leu ala ser arg ser
 181/61 211/71
 ttc tgc acc gcc atc cgc act gga atc gct taa tct ggc ccg tcg tgg tgc tgg tct tgc
 phe cys thr ala ile arg thr gly ile ala) OCH (ser gly pro ser trp cys trp ser cys)
 241/81 271/91 SEQ ID NO: 750
 tga ccg ggt tgg cgg cgt tcg ggt ccg gat tcg tca act cga cac ctt ggc agc aga tc
 OPA (pro gly trp arg arg ser gly pro asp ser ser thr arg his leu gly ser arg)
 SEQ ID NO: 751

SEQ ID Nds: 746-751

FIGURE 43B

141/185

1/1 31/11
 cgc gcg tga cat cga tga cca ggg tgc gct gtg tct gga cgt cgg cgg tgc aac ggt agt
 arg ala OPA his arg OPA (pro gly ser ala val ser gly arg arg arg ser asn gly ser
 61/21 91/31
 tgt ttc agc ggg cga cgt ggt gca ttt gcg tta act cgc gcg gag ctg gcg tcc cca aaa
 cys phe ser gly arg arg gly ala phe ala leu thr arg ala glu leu ala ser pro lys
 121/41 151/51
 gat taa ggt cgc ggg cat gag cta tcc gga gaa tgt cct ggc cgc tgg cga gca ggt cgt
 asp) OCH (gly arg gly his glu leu ser gly glu cys pro gly arg trp arg ala gly arg
 181/61 211/71
 tct gca ccg cca tcc gca ctg gaa tgc ctt aat ctg gcc cgt cgt ggt gct ggt ctt gct
 ser ala pro pro ser ala leu glu ser leu asn leu ala arg arg gly ala gly leu ala
 241/81 271/91
 gac cgg gtt ggc ggc gtt cgg gtc cgg att cgt caa ctc gac acc ttg gca gca gat c
 asp arg val gly gly val arg val arg ile arg gln leu asp thr leu ala ala asp)

SEQ ID NOS: 752-754

FIGURE 43C

Coding sequence Rv3278c predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq43A:

1/1 31/11
 atg agc tat ccg gag aat gtc ctg gcc gct ggc gag cag gtc gtt ctg cac cgc cat ccg
 (Met ser tyr pro glu asn val leu ala ala gly glu gln val val leu his arg his pro
 61/21 91/31
 cac tgg aat cgc tta atc tgg ccc gtc gtg gtg ctg gtc ttg ctg acc ggg ttg gcg gcg
 his trp asn arg leu ile trp pro val val val leu val leu leu thr gly leu ala ala
 121/41 151/51
 ttc ggg tcc gga ttc gtc aac tgc aca cct tgg cag cag atc gct aag aac gtg att cac
 phe gly ser gly phe val asn ser thr pro trp gln gln ile ala lys asn val ile his
 181/61 211/71
 gcg gtc atc tgg ggg atc tgg ttg gtg atc gtc ggc tgg ctc acg ctg tgg cca ttc ctg
 ala val ile trp gly ile trp leu val ile val gly trp leu thr leu trp pro phe leu
 241/81 271/91
 agc tgg ctg acc aca cat ttc gtg gtg acc aac cgg cgg gtg atg ttc cgg cat ggt gtg
 ser trp leu thr thr his phe val val thr asn arg arg val met phe arg his gly val
 301/101 331/111
 ctg acc cgc agc ggg atc gac ata ccg cta gca cgg atc aac agc gtg gag ttc cgg gac
 leu thr arg ser gly ile asp ile pro leu ala arg ile asn ser val glu phe arg asp
 361/121 391/131
 cgg atc ttc gag cgg att ttt cgc acc ggg acg ttg att atc gag tcc gcg tca caa gat
 arg ile phe glu arg ile phe arg thr gly thr leu ile ile glu ser ala ser gln asp
 421/141 451/151
 ccg ctc gag ttc tac aac att ccg cgc ctg ccg gag gtg cat gcg ttg ctg tat cac gag
 pro leu glu phe tyr asn ile pro arg leu arg glu val his ala leu leu tyr his glu
 481/161 511/171
 gtt ttc gac acc ctg ggc tcc gac gag tgc ccc agc tga
 val phe asp thr leu gly ser asp glu ser pro ser) OPA

SEQ ID NOS: 755-756

FIGURE 43D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv3278c

1/1 31/11
 taa ctc gcg cgg agc tgg cgt ccc caa aag att aag gtc gcg ggc atg agc tat ccg gag
 OCH (leu ala arg ser trp arg pro gln lys ile lys val ala gly met ser tyr pro glu
 61/211 **SEQ ID NO: 758** 91/31
 aat gtc ctg gcc gct ggc gag cag gtc gtt ctg cac cgc cat ccg cac tgg aat cgc tta
 asn val leu ala ala gly glu gln val val leu his arg his pro his trp asn arg leu
 121/41 151/51
 atc tgg ccc gtc gtg gtg ctg gtc ttg ctg acc ggg ttg gcg gcg ttc ggg tcc gga ttc
 ile trp pro val val val leu val leu leu thr gly leu ala ala phe gly ser gly phe
 181/61 211/71
 gtc aac tcg aca cct tgg cag cag atc gct aag aac gtg att cac gcg gtc atc tgg ggg
 val asn ser thr pro trp gln gln ile ala lys asn val ile his ala val ile trp gly
 241/81 271/91
 atc tgg ttg gtg atc gtc ggc tgg ctc acg ctg tgg cca ttc ctg agc tgg ctg acc aca
 ile trp leu val ile val gly trp leu thr leu trp pro phe leu ser trp leu thr thr
 301/101 331/111
 cat ttc gtg gtg acc aac cgg cgg gtg atg ttc cgg cat ggt gtg ctg acc cgc agc ggg
 his phe val val thr asn arg arg val met phe arg his gly val leu thr arg ser gly
 361/121 391/131
 atc gac ata ccg cta gca cgg atc aac agc gtg gag ttc cgg gac cgg atc ttc gag cgg
 ile asp ile pro leu ala arg ile asn ser val glu phe arg asp arg ile phe glu arg
 421/141 451/151
 att ttt cgc acc ggg acg ttg att atc gag tcc gcg tca caa gat ccg ctc gag ttc tac
 ile phe arg thr gly thr leu ile ile glu ser ala ser gln asp pro leu glu phe tyr
 481/161 511/171
 aac att ccg cgc ctg cgg gag gtg cat gcg ttg ctg tat cac gag gtt ttc gac acc ctg
 asn ile pro arg leu arg glu val his ala leu leu tyr his glu val phe asp thr leu
 541/181
 ggc tcc gac gag tcg ccc agc tga
 gly ser asp glu ser pro ser) OPA

SEQ ID Nos: 757-758

FIGURE 43E

143/185

EAJDND: 759
SEQ ID NO: 760

1/1	gcc aag atg gat gtc tac caa cgc acc gcc	31/11	gcc ggc tgg cag ccg ctc aag acc ggt atc
61/21	ala lys met asp val tyr gln arg thr ala	91/31	ala gly trp gln pro leu lys thr gly ile
121/41	acc acc cat atc ggt tcg gcg ggc atg gcg	151/51	ccg gaa gcc aag agc gga tat ccg gcc act
181/61	thr thr his ile gly ser ala gly met ala	211/71	pro glu ala lys ser gly tyr pro ala thr
241/81	ccg atg ggg gtt tac agc ctg gac tcc gct	271/91	ttt ggc acc gcg ccg aat ccc ggt ggc ggg
301/101	pro met gly val tyr ser leu asp ser ala	331/111	phe gly thr ala pro asn pro gly gly gly
361/121	ttg ccg tat acc caa gtc gga ccc aat cac	391/131	tgg tgg agt ggc gac gac aat agc ccc acc
421/141	leu pro tyr thr gln val gly pro asn his		trp trp ser gly asp asp asn ser pro thr
	ttt aac tcc atg cag gtc tgt cag aag tcc		cag tgc ccg ttc agc acg gcc gac agc gag
	phe asn ser met gln val cys gln lys ser		gln cys pro phe ser thr ala asp ser glu
	aac ctg caa atc ccg cag tac aag cat tcg		gtc gtg atg ggc gtc aac aag gcc aag gtc
	asn leu gln ile pro gln tyr lys his ser		val val met gly val asn lys ala lys val
	cca ggc aaa ggc tcc gcg ttc ttc ttt cac		acc acc gac ggc ggg ccc acc gcg ggt tgt
	pro gly lys gly ser ala phe phe phe his		thr thr asp gly gly pro thr ala gly cys
	gtg gcg atc		
	val ala ile		

SEQ ID NOS: 759-760

FIGURE 44A

SEQ ID NO: 761
SEQ ID NO: 762

1/1	cca aga tgg atg tct acc aac gca ccg ccg	31/11	ccg gct ggc agc cgc tca aga ccg gta tca
61/21	pro arg trp met ser thr asn ala pro pro	91/31	pro ala gly ser arg ser arg pro val ser
121/41	cca ccc ata tcg gtt cgg cgg gca tgg cgc	151/51	ccg aag cca aga gcg gat atc ccg cca ctc
181/61	pro pro ile ser val arg arg ala trp arg	211/71	arg lys pro arg ala asp ile arg pro leu
241/81	cga tgg ggg ttt aca gcc tgg act ccg ctt	271/91	ttg gca ccg cgc cga atc ccg gtg gcg ggt
301/101	arg trp gly phe thr ala trp thr pro leu	331/111	leu ala pro arg arg ile pro val ala gly
	tgc cgt ata ccc aag tcg gac cca atc act		ggt gga gtg gcg acg aca ata gcc cca cct
	cys arg ile pro lys ser asp pro ile thr		gly gly val ala thr thr ile ala pro pro
	tta act cca tgc agg tct gtc aga agt ccc		agt gcc cgt tca gca cgg ccg aca gcg aga
	leu thr pro cys arg ser val arg ser pro		ser ala arg ser ala arg pro thr ala arg
	acc tgc aaa tcc cgc agt aca agc att ccg		tcg tga tgg gcg tca aca agg cca agg tcc
	thr cys lys ser arg ser thr ser ile arg		ser OPA(trp ala ser thr arg pro arg ser
	cag gca aag gct ccg cgt tct tct ttc aca		391/131
	gln ala lys ala pro arg ser ser phe thr		SEQ ID NO: 763
	cca ccg acg gcg ggc cca ccg ccg gtt gtg		
	gln ala lys ala pro arg ser ser phe thr		
	pro pro thr ala gly pro pro arg val val		
	tggtg cga tc		
	trp arg		

SEQ ID NOS: 761-763

FIGURE 44B

1/1
 31/11
 EQ ID NO: 764 caa gat gga tgt cta cca acg cac cgc cgc cgg ctg gca gcc gct caa gac cgg tat cac
 61/21 gln asp gly cys leu pro thr his arg arg arg leu ala ala ala gln asp arg tyr his
 91/31
 EQ ID NO: 765 cac cca tat cgg ttc ggc ggg cat ggc gcc gga agc caa gag cgg ata tcc ggc cac tcc
 his pro tyr arg phe gly gly his gly ala gly ser gln glu arg ile ser gly his ser
 121/41 151/51
 gat ggg ggt tta cag cct gga ctc cgc ttt tgg cac cgc gcc gaa tcc cgg tgg cgg gtt
 asp gly gly leu gln pro gly leu arg phe trp his arg ala glu ser arg trp arg val
 181/61 211/71
 gcc gta tac cca agt cgg acc caa tca ctg gtg gag tgg cga cga caa tag ccc cac ctt
 ala val tyr pro ser arg thr gln ser leu val glu trp arg arg gln)AMB pro his leu
 241/81 271/91
 taa ctc cat gca ggt ctg tca gaa gtc cca gtg ccc gtt cag cac ggc cga cag cga gaa
 OCH(leu his ala gly leu ser glu val pro val pro val gln his gly arg gln arg glu
 301/101Y SER ID NO: 764 331/111
 cct gca aat ccc gca gta caa gca ttc ggt cgt gat ggg cgt caa caa ggc caa ggt ccc
 pro ala asn pro ala val gln ala phe gly arg asp gly arg gln gln gly gln gly pro
 361/121 391/131
 agg caa agg ctc cgc gtt ctt ctt tca cac cac cga cgg cgg g cac cgc ggg ttg tgt
 arg gln arg leu arg val leu leu ser his his arg arg arg a his arg gly leu cys
 421/141
 ggc gat c
 gly asp)

SEQ ID No. NOS: 764-766

FIGURE 44C

Coding sequence Rv0309 predicted by Cole et al., 1998 (Nature 393:537-544) and containing Seq44A:

1/1 31/11
 Seq ID NO: 767 → atg agc cga ctc cta gct ttg ctg tgc gct gcg gta tgc acg ggc tgc gtt gct gtg gtt
 Seq ID NO: 768 → Met ser arg leu leu ala leu leu cys ala ala val cys thr gly cys val ala val val
 61/21 91/31
 ctc gcg cca gtg agc ctg gcc gtc gtc aac ccg tgg ttc gcg aac tcg gtc ggc aat gcc
 leu ala pro val ser leu ala val val asn pro trp phe ala asn ser val gly asn ala
 121/41 151/51
 act cag gtg gtt tcg gtg gtg gga acc ggc ggt tcg acg gcc aag atg gat gtc tac caa
 thr gln val val ser val val gly thr gly gly ser thr ala lys met asp val tyr gln
 181/61 211/71
 cgc acc gcc gcc gcc tgg cag ccg ctc aag acc ggt atc acc acc cat atc ggt tcg gcg
 arg thr ala ala gly trp gln pro leu lys thr gly ile thr thr his ile gly ser ala
 241/81 271/91
 gcc atg gcg ccg gaa gcc aag agc gga tat ccg gcc act ccg atg ggg gtt tac agc ctg
 gly met ala pro glu ala lys ser gly tyr pro ala thr pro met gly val tyr ser leu
 301/101 331/111
 gac tcc gct ttt ggc acc gcg ccg aat ccc ggt ggc ggg ttg ccg tat acc caa gtc gga
 asp ser ala phe gly thr ala pro asn pro gly gly gly leu pro tyr thr gln val gly
 361/121 391/131
 ccc aat cac tgg tgg agt ggc gac gac aat agc ccc acc ttt aac tcc atg cag gtc tgt
 pro asn his trp trp ser gly asp asp asn ser pro thr phe asn ser met gln val cys
 421/141 451/151
 cag aag tcc cag tgc ccg ttc agc acg gcc gac agc gag aac ctg caa atc ccg cag tac
 gln lys ser gln cys pro phe ser thr ala asp ser glu asn leu gln ile pro gln tyr
 481/161 511/171
 aag cat tcg gtc gtg atg ggc gtc aac aag gcc aag gtc cca ggc aaa ggc tcc gcg ttc
 lys his ser val val met gly val asn lys ala lys val pro gly lys gly ser ala phe
 541/181 571/191
 ttc ttt cac acc acc gac ggc ggg ccc acc gcg ggt tgt gtg gcg atc gac gat gcc acg
 phe phe his thr thr asp gly gly pro thr ala gly cys val ala ile asp asp ala thr
 601/201 631/211
 ctg gtg cag atc atc cgt tgg ctg cgg cct ggt gcg gtg atc gcg atc gcc aag taa
 leu val gln ile ile arg trp leu arg pro gly ala val ile ala ile ala lys) OCH

SEQ ID NOS: 767-768

FIGURE 44D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0309

1/1
 tga gcg atg agc cga ctc cta gct ttg ctg tgc gct gcg gta tgc acg ggc tgc gtt gct
 OPA(ala met ser arg leu leu ala leu leu cys ala ala val cys thr gly cys val ala
 61/21
 61/21
 gtg gtt ctc gcg cca gtg agc ctg gcc gtc gtc aac ccg tgg ttc gcg aac tcg gtc ggc
 val val leu ala pro val ser leu ala val val asn pro trp phe ala asn ser val gly
 121/41
 121/41
 aat gcc act cag gtg gtt tcg gtg gtg gga acc ggc ggt tcg acg gcc aag atg gat gtc
 asn ala thr gln val val ser val val gly thr gly gly ser thr ala lys met asp val
 181/61
 181/61
 tac caa cgc acc gcc gcc gcc ggc tgg cag ccg ctc aag acc ggt atc acc acc cat atc ggt
 tyr gln arg thr ala ala gly trp gln pro leu lys thr gly ile thr thr his ile gly
 241/81
 241/81
 tcg gcg ggc atg gcg ccg gaa gcc aag agc gga tat ccg gcc act ccg atg ggg gtt tac
 ser ala gly met ala pro glu ala lys ser gly tyr pro ala thr pro met gly val tyr
 301/101
 301/101
 agc ctg gac tcc gct ttt ggc acc gcg ccg aat ccc ggt ggc ggg ttg ccg tat acc caa
 ser leu asp ser ala phe gly thr ala pro asn pro gly gly gly leu pro tyr thr gln
 361/121
 361/121
 gtc gga ccc aat cac tgg tgg agt ggc gac gac aat agc ccc acc ttt aac tcc atg cag
 val gly pro asn his trp trp ser gly asp asp asn ser pro thr phe asn ser met gln
 421/141
 421/141
 gtc tgt cag aag tcc cag tgc ccg ttc agc acg gcc gac agc gag aac ctg caa atc ccg
 val cys gln lys ser gln cys pro phe ser thr ala asp ser glu asn leu gln ile pro
 481/161
 481/161
 cag tac aag cat tcg gtc gtg atg ggc gtc aac aag gcc aag gtc cca ggc aaa ggc tcc
 gln tyr lys his ser val val met gly val asn lys ala lys val pro gly lys gly ser
 541/181
 541/181
 gcg ttc ttc ttt cac acc acc gac ggc ggc ccc acc gcg ggt tgt gtg gcg atc gac gat
 ala phe phe phe his thr thr asp gly gly pro thr ala gly cys val ala ile asp asp
 601/201
 601/201
 gcc acg ctg gtg cag atc atc cgt tgg ctg ccg cct ggt gcg gtg atc gcg atc gcc aag
 ala thr leu val gln ile ile arg trp leu arg pro gly ala val ile ala ile ala lys)
 661/221
 661/221
 taa
 OCH

SEQ ID NDS: 769-770

FIGURE 44F

Cloned fragment fused with phoA

1/1

31/11

SEQ ID NO: 771 → gat ctc ccc gga cac cag gtc atc cgg cga gat ggt gat cga ggc tcg gac ccg cag gca
 SEQ ID NO: 772 → (asp leu pro gly his gln val ile arg arg asp gly asp arg gly ser asp pro gln ala
 61/21 91/31

tcc ggt agc cag agg cac cag cat cag caa cat cgc gat ggc cag cat gcc gcg ccg tcg
 ser gly ser gln arg his gln his gln gln his arg asp gly gln his ala ala pro ser
 121/41 151/51

ggt cct tgc cac tcg cga tcc ttg gga tga cgg tgg ggc ata gct agc gcg cac cag gtc
 gly pro cys his ser arg ser leu gly) OPA (arg trp gly ile ala ser ala his gln val
 181/61 211/71

atc gtg cca gac cgg gca tgc cgc gtc gcc aag ctg tcg ggc gcg ggt tag agc ggt agc
 ile val pro asp arg ala cys arg val gly lys leu ser gly ala gly) AMB (ser gly ser
 241/81 271/91

gtg cga ccc agg atg gcg aat gct cgg ggg tca ccg gcg aag tgg tag ccg cgg atg atg
 val arg pro arg met ala asn ala arg gly ser pro ala lys trp) AMB (pro arg met met
 301/101 331/111

tcg gtg aag ccc aac cgg cgg tac aac cgc cac gcc cga ttg tcc tca ccg ttg gtc tcc
 ser val lys pro asn arg arg tyr asn arg his ala arg leu ser ser pro leu val ser
 361/121 391/131

ggt gtg gag agc agg acg ttg tcc tcg tcg cga ccg gct agc agt cgg cgg gcc aac gcc
 gly val glu ser arg thr leu ser ser ser arg pro ala ser ser arg arg ala asn ala
 421/141 451/151

tcc ccg agg cca cgg cct tga gcg cgg gga agg atg tgc aat tca gtc aac tcg aag tag
 ser pro arg pro arg pro) OPA (ala arg gly arg met cys asn ser val asn ser lys) AMB
 481/161 511/171

ctg gtc atc agt cgg gcg atc gct agg cgc gga aag ccg ctg cgt tgc aag ccc agt acc
 (leu val ile ser arg ala ile ala arg arg gly lys pro leu arg cys lys pro ser thr
 541/181 571/191

acc tgc tgt tgc cac cac tgg ccg gcc gcc ccg gga tag ccg tac gcc act ccg agc att
 thr cys cys cys his his trp pro gly ala pro gly) AMB (pro tyr ala thr pro ser ile
 601/201 631/211

ggc gcg ttg ctc agt tcg gcg gcc gac gcc agc gcc gtg gtg tcg gcg gcc tcg gcc tgt
 gly ala leu leu ser ser ala ala asp gly ser ala val val ser ala ala ser ala cys
 661/221 691/231

tcg gct gcc gtt acc tcg acg gcc gcg acc gcc tgc cag ccg cgc cgc cgg atg tgc tcc
 ser ala ala val thr ser thr ala ala thr ala cys gln pro arg arg arg met cys ser
 721/241 751/251

agc cac att ggg gcg cgc aaa gtc tcg gtg ccc ctg ggg tag cgc atc gcg tcg aca tac
 ser his ile gly ala arg lys val ser val pro leu gly) AMB (arg ile ala ser thr tyr
 781/261 811/271

acc gtc agg gca tca ccg agg cgg cgc tcc ata tcg ctg gcc gcc aga tcg atg agg aat
 thr val arg ala ser pro arg arg arg ser ile ser leu gly gly arg ser met arg asn
 841/281 871/291

atc gcc aac gcg cgg tgt cct cct cat gtg atg aac cga tgc gtg ctt gcg cac cag tat
 ile ala asn ala arg cys pro pro his val met asn arg cys val leu ala his gln tyr
 901/301 931/311

cgg aca agc cga tga ggc cgc ccg cgc tgg acg ggg ctt gta gcg tat gcc cgt ttc cgc
 arg thr ser arg) OPA (gly arg pro arg trp thr gly leu val ala tyr gly arg phe arg
 SEQ ID NO: 780

SEQ ID NOS: 771-783

FIGURE 45ZA

961/321	991/331
tca gct cgt cgc tgc ggc gcc gcc ggg ata	gaa tcg ccc gcg aac cag tgg tac ggc gca
ser ala arg arg cys gly ala ala gly ile	glu ser pro ala asn gln trp tyr gly ala
1021/341	1051/351
gat tga cct cgt atc atc tga gtt agt tgc	ccg cgc aat ggg cat ccg cgt gtt atc ggt
asp) OPA (pro arg ile ile) OPA (val ser cys	pro arg asn gly his pro arg val ile gly
1081/361	1111/371
att acg tga cag tct gtc ggc aag gag gga	cgc atg cca ctc tcc gat cat gag cag cgg
ile thr) OPA (gln ser val gly lys glu gly	arg met pro leu ser asp his glu gln arg
1141/381	1171/391
atg ctt gac cag atc gag agc gct ctc tac	gcc gaa gat ccc aag ttc gca tcg agt gtc
met leu asp gln ile glu ser ala leu tyr	ala glu asp pro lys phe ala ser ser val
1201/401	1231/411
cgt ggc ggg ggc ttc cgc gca ccg acc gcg	cgg cgg cgc ctg cag ggc gcg gcg ttg ttc
arg gly gly gly phe arg ala pro thr ala	arg arg arg leu gln gly ala ala leu phe
1261/421	1291/431
atc atc ggt ctg ggg atg ttg gtt tcc ggc	gtg gcg ttc aaa gag acc atg atc gga agt
ile ile gly leu gly met leu val ser gly	val ala phe lys glu thr met ile gly ser
1321/441	1351/451
ttc ccg ata ctc agc gtt ttc ggt ttt gtc	gtg atg ttc ggt ggt gtg gtg tat gcc atc
phe pro ile leu ser val phe gly phe val	val met phe gly gly val val tyr ala ile
1381/461	1411/471
acc ggt cct cgg ttg tcc ggc agg atg gat	cgt ggc gga tcg gct gct ggg gct tcg cgc
thr gly pro arg leu ser gly arg met asp	arg gly gly ser ala ala gly ala ser arg
1441/481	1471/491
cag cgt cgt acc aag ggg gcc ggg ggc tca	ttc acc agc cgt atg gaa gat c
gln arg arg thr lys gly ala gly gly ser	phe thr ser arg met glu asp)

SEQ ID NOS:771- (continued)
783

FIGURE 45ZA (continued)

149/185

fragment seq45ZA shifted minus 1 for the reading frame

1/1 → **SEQ ID NO: 784** 31/11
 atc tcc ccg gac acc agg tca tcc ggc gag atg gtg atc gag gct cgg acc cgc agg cat
 ile ser pro asp thr arg ser ser gly glu met val ile glu ala arg thr arg arg his
 61/21 91/31
 ccg gta gcc aga ggc acc agc atc agc aac atc gcg atg gcc agc atg ccg cgc cgt cgg
 pro val ala arg gly thr ser ile ser asn ile ala met ala ser met pro arg arg arg
 121/41 151/51
 gtc ctt gcc act cgc gat cct tgg gat gac ggt ggg gca tag cta gcg cgc acc agg tca
 val leu ala thr arg asp pro trp asp asp gly gly ala) **AMB** (leu ala arg thr arg ser
 181/61 211/71 **SEQ ID NO: 786**
 tcg tgc cag acc ggg cat gcc gcg tcg gca agc tgt cgg gcg cgg gtt aga gcg gta gcg
 ser cys gln thr gly his ala ala ser ala ser cys arg ala arg val arg ala val ala
 241/81 271/91
 tgc gac cca gga tgg cga atg ctc ggg ggt cac cgg cga agt ggt agc cgc gga tga tgt
 cys asp pro gly trp arg met leu gly gly his arg arg ser gly ser arg gly) **OPA** cys
 301/101 331/111
 cgg tga agc cca acc ggc ggt aca acc gcc acg ccc gat tgt cct cac cgt tgg tct ccg
 arg **OPA** (ser pro thr gly gly thr thr ala thr pro asp cys pro his arg trp ser pro
 361/121 **SEQ ID NO: 787** 391/131
 gtg tgg aga gca gga cgt tgt cct cgt cgc gac cgg cta gca gtc ggc ggg cca acg cct
 val trp arg ala gly arg cys pro arg arg asp arg leu ala val gly gly pro thr pro
 421/141 451/151
 ccc cga ggc cac ggc ctt gag cgc ggg gaa gga tgt gca att cag tca act cga agt agc
 pro arg gly his gly leu glu arg gly glu gly cys ala ile gln ser thr arg ser ser
 481/161 511/171
 tgg tca tca gtc ggg cga tcg cta ggc gcg gaa agc cgc tgc gtt gca agc cca gta cca
 trp ser ser val gly arg ser leu gly ala glu ser arg cys val ala ser pro val pro
 541/181 571/191
 cct gct gtt gcc acc act ggc cgg gcg ccc cgg gat agc cgt acg cca ctc cga gca ttg
 pro ala val ala thr thr gly arg ala pro arg asp ser arg thr pro leu arg ala leu
 601/201 631/211
 gcg cgt tgc tca gtt cgg cgg ccg acg gca gcg ccg tgg tgt cgg cgg cct cgg cct gtt
 ala arg cys ser val arg arg pro thr ala ala pro trp cys arg arg pro arg pro val
 661/221 691/231
 cgg ctg ccg tta cct cga cgg ccg cga ccg cct gcc agc cgc gcc gcc gga tgt gct cca
 arg leu pro leu pro arg arg pro arg pro pro ala ser arg ala ala gly cys ala pro
 721/241 751/251
 gcc aca ttg ggg cgc gca aag tct cgg tgc ccc tgg ggt agc gca tcg cgt cga cat aca
 ala thr leu gly arg ala lys ser arg cys pro trp gly ser ala ser arg arg his thr
 781/261 811/271
 ccg tca ggg cat cac cga ggc ggc gct cca tat cgc tgg gcg gca gat cga tga gga ata
 pro ser gly his his arg gly gly ala pro tyr arg trp ala ala asp arg) **OPA** (gly ile
 841/281 871/291 **SEQ ID NO: 788**
 tcg cca acg cgc ggt gtc ctc ctc atg tga tga acc gat gcg tgc ttg cgc acc agt atc
 ser pro thr arg gly val leu leu met) **OPA** **OPA** (thr asp ala cys leu arg thr ser ile
 901/301 931/311 **SEQ ID NO: 789**
 gga caa gcc gat gag gcc gcc cgc gct gga cgg ggc ttg tag cgt atg gcc gtt tcc gct
 gly gln ala asp glu ala ala arg ala gly arg gly leu) **AMB** (arg met ala val ser ala
 961/321 991/331 **SEQ ID NO: 790**
 cag ctc gtc gct gcg gcg ccg ccg gga tag aat cgc ccg cga acc agt ggt acg gcg cag
 gln leu val ala ala ala pro pro gly) **AMB** (asn arg pro arg thr ser gly thr ala gln
SEQ ID NO: 791

SEQ ID NDS: 784-793

FIGURE 45ZB

1021/341
 att gac ctc gta tca tct gag tta gtt gcc cgc gca atg ggc atc cgc gtg tta tcg gta
 ile asp leu val ser ser glu leu val ala arg ala met gly ile arg val leu ser val
 1081/361
 tta cgt gac agt ctg tcg gca agg agg gac gca tgc cac tct ccg atc atg agc agc gga
 leu arg asp ser leu ser ala arg arg asp ala cys his ser pro ile met ser ser gly
 1141/381
 tgc ttg acc aga tcg aga gcg ctc tct acg ccg aag atc cca agt tcg cat cga gtg tcc
 cys leu thr arg ser arg ala leu ser thr pro lys ile pro ser ser his arg val ser
 1201/401
 gtg gcg ggg gct tcc gcg cac cga ccg cgc ggc ggc gcc tgc agg gcg cgg cgt tgt tca
 val ala gly ala ser ala his arg pro arg gly gly ala cys arg ala arg arg cys ser
 1261/421
 tca tcg gtc tgg gga tgt tgg ttt ccg gcg tgg cgt tca aag aga cca tga tcg gaa gtt
 ser ser val trp gly cys trp phe pro ala trp arg ser lys arg pro) OPA (ser glu val
 1321/441
 tcc cga tac tca gcg ttt tcg gtt ttg tcg tga tgt tcg gtg gtg tgg tgt atg cca tca
 ser arg tyr ser ala phe ser val leu ser) OPA (cys ser val val trp cys met pro ser
 1381/461
 ccg gtc ctc ggt tgt ccg gca gga tgg atc gtg gcg gat ccg ctg ctg ggg ctt cgc gcc
 pro val leu gly cys pro ala gly trp ile val ala asp arg leu leu gly leu arg ala
 1441/481
 agc gtc gta cca agg ggg ccg ggg gct cat tca cca gcc gta tgg aag atc
 ser val val pro arg gly pro gly ala his ser pro ala val trp lys ile)

SEQ ID NO: 784-793 (continued)

FIGURE 452B (continued)

151/185

fragment seq45ZA shifted minus 2 for the reading frame

1/1 SEQ ID NO: 794

31/11

tct ccc cgg aca cca ggt cat ccg gcg aga tgg tga tcg agg ctc gga ccc gca ggc atc
 ser pro arg thr pro gly his pro ala arg trp) OPA (ser arg leu gly pro ala gly ile
 61/21 91/31
 cgg tag cca gag gca cca gca tca gca aca tcg cga tgg cca gca tgc cgc gcc gtc ggg
 arg) AMB (pro glu ala pro ala ser ala thr ser arg trp pro ala cys arg ala val gly
 121/41 151/51
 tcc ttg cca ctc gcg atc ctt ggg atg acg gtg ggg cat agc tag cgc gca cca ggt cat
 ser leu pro leu ala ile leu gly met thr val gly his ser) AMB (arg ala pro gly his
 181/61 211/71
 cgt gcc aga ccg ggc atg ccg cgt cgg caa gct gtc ggg cgc ggg tta gag cgg tag cgt
 arg ala arg pro gly met pro arg arg gln ala val gly arg gly leu glu arg) AMB (arg
 241/81 271/91
 gcg acc cag gat ggc gaa tgc tcg ggg gtc acc ggc gaa gtg gta gcc gcg gat gat gtc
 ala thr gln asp gly glu cys ser gly val thr gly glu val val ala ala asp asp val
 301/101 331/111
 ggt gaa gcc caa ccg gcg gta caa ccg cca cgc ccg att gtc ctc acc gtt ggt ctc cgg
 gly glu ala gln pro ala val gln pro pro arg pro ile val leu thr val gly leu arg
 361/121 391/131
 tgt gga gag cag gac gtt gtc ctc gtc gcg acc ggc tag cag tcg gcg ggc caa cgc ctc
 cys gly glu gln asp val val leu val ala thr gly) AMB (gln ser ala gly gln arg leu
 421/141 451/151
 ccc gag gcc acg gcc ttg agc gcg ggg aag gat atg cca ttc agt caa ctc gaa gta gct
 pro glu ala thr ala leu ser ala gly lys asp val gln phe ser gln leu glu val ala
 481/161 511/171
 ggt cat cag tcg ggc gat cgc tag gcg cgg aaa gcc gct gcg ttg caa gcc cag tac cac
 gly his gln ser gly asp arg) AMB (ala arg lys ala ala ala leu gln ala gln tyr his
 541/181 571/191
 ctg ctg ttg cca cca ctg gcc ggg cgc ccc ggg ata gcc gta cgc cac tcc gag cat tgg
 leu leu leu pro pro leu ala gly arg pro gly ile ala val arg his ser glu his trp
 601/201 631/211
 cgc gtt gct cag ttc ggc ggc cga cgg cag cgc cgt ggt gtc ggc ggc ctc ggc ctg ttc
 arg val ala gln phe gly gly arg arg gln arg arg gly val gly gly leu gly leu phe
 661/221 691/231
 ggc tgc cgt tac ctc gac ggc cgc gac cgc ctg cca gcc gcg ccg ccg gat gtg ctc cag
 gly cys arg tyr leu asp gly arg asp arg leu pro ala ala pro pro asp val leu gln
 721/241 751/251
 cca cat tgg ggc gcg caa agt ctc ggt gcc cct ggg gta gcg cat cgc gtc gac ata cac
 pro his trp gly ala gln ser leu gly ala pro gly val ala his arg val asp ile his
 781/261 811/271
 cgt cag ggc atc acc gag gcg gcg ctc cat atc gct ggg cgg cag atc gat gag gaa tat
 arg gln gly ile thr glu ala ala leu his ile ala gly arg gln ile asp glu glu tyr
 841/281 871/291
 cgc caa cgc gcg gtg tcc tcc tca tgt gat gaa ccg atg cgt gct tgc gca cca gta tcg
 arg gln arg ala val ser ser ser cys asp glu pro met arg ala cys ala pro val ser
 901/301 931/311
 gac aag ccg atg agg ccg ccc gcg ctg gac ggg gct tgt agc gta tgg ccg ttt ccg ctc
 asp lys pro met arg pro pro ala leu asp gly ala cys ser val trp pro phe pro leu

SEQ ID NOS: 794-804

FIGURE 45ZC

152/185

961/321
 agc tcg tcg ctg cgg cgc cgc cgg gat aga atc gcc cgc gaa cca gtg gta cgg cgc aga
 ser ser ser leu arg arg arg arg asp arg ile ala arg glu pro val val arg arg arg
 1021/341
 ttg acc tcg tat cat ctg agt tag ttg ccc cgc caa tgg gca tcc gcg tgt tat cgg tat
 leu thr ser tyr his leu ser) AMB (leu pro ala gln trp ala ser ala cys tyr arg tyr
 1081/361
 tac gtg aca gtc tgt cgg caa gga ggg acg cat gcc act ctc cga tca tga gca gcg gat
 tyr val thr val cys arg gln gly gly thr his ala thr leu arg ser) OPA (ala ala asp
 1141/381
 gct tga cca gat cga gag cgc tct cta cgc cga aga tcc caa gtt cgc atc gag tgt ccg
 ala) OPA (pro asp arg glu arg ser leu arg arg arg ser gln val arg ile glu cys pro
 1201/401
 tgg cgg ggg ctt ccg cgc acc gac cgc gcg gcg gcg cct gca ggg cgc ggc gtt gtt cat
 trp arg gly leu pro arg thr asp arg ala ala ala pro ala gly arg gly val val his
 1261/421
 cat cgg tct ggg gat gtt ggt ttc cgg cgt ggc gtt caa aga gac cat gat cgg aag ttt
 his arg ser gly asp val gly phe arg arg gly val gln arg asp his asp arg lys phe
 1321/441
 ccc gat act cag cgt ttt cgg ttt tgt cgt gat gtt cgg tgg tgt ggt gta tgc cat cac
 pro asp thr gln arg phe arg phe cys arg asp val arg trp cys gly val cys his his
 1381/461
 cgg tcc tcg gtt gtc cgg cag gat gga tcg tgg cgg atc ggc tgc tgg ggc ttc gcg cca
 arg ser ser val val arg gln asp gly ser trp arg ile gly cys trp gly phe ala pro
 1441/481
 gcg tcg tac caa ggg ggc cgg ggg ctc att cac cag ccg tat gga aga tc
 ala ser tyr gln gly gly arg gly leu ile his gln pro tyr gly arg)

SEQ ID NOS: 794-804 (continued 1)

FIGURE 45ZC (continued 1)

seq 45ZA joined directly to phoA

SEQ ID NO: 805

SEQ ID NO: 806

cag tct gtc ggc aag gag gga cgc atg cca ctc tcc gat cat gag cag cgg
 gln ser val gly lys glu gly arg met pro leu ser asp his glu gln arg
 1141/381
 atg ctt gac cag atc gag agc gct ctc tac gcc gaa gat ccc aag ttc gca tcg agt gtc
 met leu asp gln ile glu ser ala leu tyr ala glu asp pro lys phe ala ser ser val
 1201/401
 cgt ggc ggg ggc ttc cgc gca ccg acc gcg cgg cgg cgc ctg cag ggc gcg gcg ttg ttc
 arg gly gly gly phe arg ala pro thr ala arg arg arg leu gln gly ala ala leu phe
 1261/421
 atc atc ggt ctg ggg atg ttg gtt tcc ggc gtg gcg ttc aaa gag acc atg atc gga agt
 ile ile gly leu gly met leu val ser gly val ala phe lys glu thr met ile gly ser
 1321/441
 ttc ccg ata ctc agc gtt ttc ggt ttt gtc gtg atg ttc ggt ggt gtg gtg tat gcc atc
 phe pro ile leu ser val phe gly phe val val met phe gly gly val val tyr ala ile
 1381/461
 acc ggt cct cgg ttg tcc ggc agg atg gat cgt ggc gga tcg gct gct ggg gct tcg cgc
 thr gly pro arg leu ser gly arg met asp arg gly gly ser ala ala gly ala ser arg
 1441/481
 cag cgt cgt acc aag ggg gcc ggg ggc tca ttc acc agc cgt atg gaa gat c
 gln arg arg thr lys gly ala gly gly ser phe thr ser arg met glu asp)

SEQ ID NOS: 805-806

FIGURE 45A

153/185

Sequence Rv2169c predicted by Cole et al., 1998 (Nature 393:537-544) and containing Seq45A

1/1

31/11

atg cca ctc tcc gat cat gag cag cgg atg ctt gac cag atc gag agc gct ctc tac gcc

Met pro leu ser asp his glu gln arg met leu asp gln ile glu ser ala leu tyr ala

61/21

91/31

gaa gat ccc aag ttc gca tcg agt gtc cgt ggc ggg ggc ttc cgc gca ccg acc gcg cgg

glu asp pro lys phe ala ser ser val arg gly gly gly phe arg ala pro thr ala arg

121/41

151/51

cgg cgc ctg cag ggc gcg gcg ttg ttc atc atc ggt ctg ggg atg ttg gtt tcc ggc gtg

arg arg leu gln gly ala ala leu phe ile ile gly leu gly met leu val ser gly val

181/61

211/71

gcg ttc aaa gag acc atg atc gga agt ttc ccg ata ctc agc gtt ttc ggt ttt gtc gtg

ala phe lys glu thr met ile gly ser phe pro ile leu ser val phe gly phe val val

241/81

271/91

atg ttc ggt ggt gtg gtg tat gcc atc acc ggt cct cgg ttg tcc ggc agg atg gat cgt

met phe gly gly val val tyr ala ile thr gly pro arg leu ser gly arg met asp arg

301/101

331/111

ggc gga tcg gct gct ggg gct tcg cgc cag cgt cgt acc aag ggg gcc ggg ggc tca ttc

gly gly ser ala ala gly ala ser arg gln arg arg thr lys gly ala gly gly ser phe

361/121

391/131

acc agc cgt atg gaa gat cgg ttc cgg cgc cgc ttc gac gag taa

thr ser arg met glu asp arg phe arg arg arg phe asp glu)OCH

SEQ ID NOS: 807-808

FIGURE 45D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv2169c

1/1

31/11

tga cag tct gtc ggc aag gag gga cgc atg cca ctc tcc gat cat gag cag cgg atg ctt

OPA (gln ser val gly lys glu gly arg met pro leu ser asp his glu gln arg met leu

61/21

91/31

gac cag atc gag agc gct ctc tac gcc gaa gat ccc aag ttc gca tcg agt gtc cgt ggc

asp gln ile glu ser ala leu tyr ala glu asp pro lys phe ala ser ser val arg gly

121/41

151/51

ggg ggc ttc cgc gca ccg acc gcg cgg cgg cgc ctg cag ggc gcg gcg ttg ttc atc atc

gly gly phe arg ala pro thr ala arg arg arg leu gln gly ala ala leu phe ile ile

181/61

211/71

ggt ctg ggg atg ttg gtt tcc ggc gtg gcg ttc aaa gag acc atg atc gga agt ttc ccg

gly leu gly met leu val ser gly val ala phe lys glu thr met ile gly ser phe pro

241/81

271/91

ata ctc agc gtt ttc ggt ttt gtc gtg atg ttc ggt ggt gtg gtg tat gcc atc acc ggt

ile leu ser val phe gly phe val val met phe gly gly val val tyr ala ile thr gly

301/101

331/111

cct cgg ttg tcc ggc agg atg gat cgt ggc gga tcg gct gct ggg gct tcg cgc cag cgt

pro arg leu ser gly arg met asp arg gly gly ser ala ala gly ala ser arg gln arg

361/121

391/131

cgt acc aag ggg gcc ggg ggc tca ttc acc agc cgt atg gaa gat cgg ttc cgg cgc cgc

arg thr lys gly ala gly gly ser phe thr ser arg met glu asp arg phe arg arg arg

421/141

ttc gac gag taa

phe asp glu)OCH

SEQ ID NOS: 809-810

FIGURE 45E

154/185

1/1 31/11
 EQ ID NO: 811 → cag cgc cgc cgc atc gac cag ggc ctc acg ccc ggt cac ttc tcc gcg ttc ctc aac aat
 EQ ID NO: 812 → gln pro arg arg ile asp gln gly leu thr pro gly his phe ser ala phe leu asn asn
 61/21 91/31
 tcc ggt gaa cat cgc acc agg tta ggc agc aat ccc gcg gac ccg cac ccc act cgc cga
 ser gly glu his arg thr arg leu gly ser asn pro ala asp pro his pro thr arg arg
 121/41 151/51
 ccg gcc aac tca cag aca ccc tct acg atg cag ggt atg ccg acc ccc aga cgc cac tgc
 pro ala asn ser gln thr pro ser thr met gln gly met arg thr pro arg arg his cys
 181/61 211/71
 cgt cgc atc gcc gtc ctc gcc gcc gtt agc atc gcc gcc act gtc gtt gcc gcc tgc tgc
 arg arg ile ala val leu ala ala val ser ile ala ala thr val val ala gly cys ser
 241/81 271/91
 tcg gcc tcg aag cca agc ggc gga cca ctt ccg gac gcg aag ccg ctg gtc gag gag gcc
 ser gly ser lys pro ser gly gly pro leu pro asp ala lys pro leu val glu glu ala
 301/101 331/111
 acc gcg cag acc aag gct ctc aag agc gcg cac atg gtg ctg acg gtc aac gcc aag atc
 thr ala gln thr lys ala leu lys ser ala his met val leu thr val asn gly lys ile)

SEQ ID NOS: 811-812

FIGURE 46A

1/1 31/11
 EQ ID NO: 813 → agc cgc gcc gca tcg acc agg gcc tca cgc ccg gtc act tct ccg cgt tcc tca aca att
 EQ ID NO: 814 → ser arg ala ala ser thr arg ala ser arg pro val thr ser pro arg ser ser thr ile
 61/21 91/31
 ccg gtg aac atc gca cca ggt tag gca gca atc ccg ccg acc cgc acc cca ctc gcc gac
 pro val asn ile ala pro gly) AMB(ala ala ile pro arg thr arg thr pro leu ala asp
 121/41 151/51
 ccg cca act cac aga cac cct cta cga tgc agg gta tgc gga ccc cca gac gcc act gcc
 arg pro thr his arg his pro leu arg cys arg val cys gly pro pro asp ala thr ala
 181/61 211/71
 gtc gca tcg ccg tcc tcg ccg ccg tta gca tcg ccg cca ctg tcg ttg ccg gct gct cgt
 val ala ser pro ser ser pro pro leu ala ser pro pro leu ser leu pro ala ala arg
 241/81 271/91
 ccg gct cga agc caa gcg gcg gac cac ttc ccg acg cga agc cgc tgg tcg agg agg cca
 arg ala arg ser gln ala ala asp his phe arg thr arg ser arg trp ser arg arg pro
 301/101 331/111
 ccg cgc aga cca agg ctc tca aga gcg cgc aca tgg tgc tga ccg tca acg gca aga tc
 pro arg arg pro arg leu ser arg ala arg thr trp cys) OPA(arg ser thr ala arg)
 SEQ ID NO: 816

SEQ ID NOS: 813-816

FIGURE 46B

1/1
 gcc gcg ccg cat cga cca ggg cct cac gcc 31/11
 ala ala pro his arg pro gly pro his ala arg ser leu leu arg val pro gln gln phe
 61/21
 cgg tga aca tcg cac cag gtt agg cag caa tcc cgc gga ccc gca ccc cac tcg ccg acc
 arg) OPA (thr ser his gln val arg gln gln ser arg gly pro ala pro his ser pro thr
 121/41 SEQ ID NO: 819 151/51
 ggc caa ctc aca gac acc ctc tac gat gca ggg tat gcg gac ccc cag acg cca ctg ccg
 gly gln leu thr asp thr leu tyr asp ala gly tyr ala asp pro gln thr pro leu pro
 181/61 211/71
 tcg cat cgc cgt cct cgc cgc cgt tag cat cgc cgc cac tgt cgt tgc cgg ctg ctc gtc
 ser his arg arg pro arg arg arg) AMB (his arg arg his cys arg cys arg leu leu val
 241/81 SEQ ID NO: 820 271/91
 ggg ctc gaa gcc aag cgg cgg acc act tcc gga cgc gaa gcc gct ggt cga gga ggc cac
 gly leu glu ala lys arg arg thr thr ser gly arg glu ala ala gly arg gly gly his
 301/101 331/111
 cgc gca gac caa ggc tct caa gag cgc gca cat ggt gct gac ggt caa cgg caa gat c
 arg ala asp gln gly ser gln glu arg ala his gly ala asp gly gln arg gln asp)

SEQ ID NOS: 817-820

FIGURE 46C

Coding sequence Rv1411c predicted by Cole et al., 1998 (Nature 393: 537-544) and containing seq46A:

1/1
 31/11
 121/41
 151/51
 181/61
 211/71
 241/81
 271/91
 301/101
 331/111
 361/121
 391/131
 421/141
 451/151
 481/161
 511/171
 541/181
 571/191
 601/201
 631/211
 661/221
 691/231

atg cgg acc ccc aga cgc cac tgc cgt cgc atc gcc gtc ctc gcc gcc gtt agc atc gcc
 Met arg thr pro arg arg his cys arg arg ile ala val leu ala ala val ser ile ala
 gcc act gtc gtt gcc ggc tgc tgc tgc ggc tgc aag cca agc ggc gga cca ctt ccg gac
 ala thr val val ala gly cys ser ser gly ser lys pro ser gly gly pro leu pro asp
 gcg aag ccg ctg gtc gag gag gcc acc gcg cag acc aag gct ctc aag agc gcg cac atg
 ala lys pro leu val glu glu ala thr ala gln thr lys ala leu lys ser ala his met
 gtg ctg acg gtc aac ggc aag atc ccg gga ctg tct ctg aag acg ctg agc ggc gat ctc
 val leu thr val asn gly lys ile pro gly leu ser leu lys thr leu ser gly asp leu
 acc acc aac ccc acc gcc gcg acg gga aac gtc aag ctc acg ctg ggt ggg tct gat atc
 thr thr asn pro thr ala ala thr gly asn val lys leu thr leu gly gly ser asp ile
 gat gcc gac ttc gtg gtg ttc gac ggg atc ctg tac gcc acc ctg acg ccc aac cag tgg
 asp ala asp phe val val phe asp gly ile leu tyr ala thr leu thr pro asn gln trp
 agc gat ttc ggt ccc gcc gcc gac atc tac gac ccc gcc cag gtg ctg aat ccg gat acc
 ser asp phe gly pro ala ala asp ile tyr asp pro ala gln val leu asn pro asp thr
 ggc ctg gcc aac gtg ctg gcg aat ttc gcc gac gca aaa gcc gaa ggg ccg gat acc atc
 gly leu ala asn val leu ala asn phe ala asp ala lys ala glu gly arg asp thr ile
 aac ggc cag aac acc atc cgc atc agc ggg aag gta tgc gca cag gcg gtg aac cag ata
 asn gly gln asn thr ile arg ile ser gly lys val ser ala gln ala val asn gln ile
 gcg ccg ccg ttc aac gcg acg cag ccg gtg ccg gcg acc gtc tgg att cag gag acc ggc
 ala pro pro phe asn ala thr gln pro val pro ala thr val trp ile gln glu thr gly
 gat cat caa ctg gca cag gcc cag ttg gac cgc ggc tgc ggc aat tcc gtc cag atg acc
 asp his gln leu ala gln ala gln leu asp arg gly ser gly asn ser val gln met thr
 ttg tgc aaa tgg ggc gag aag gtc cag gtc acg aag ccc ccg gtg agc tga
 leu ser lys trp gly glu lys val gln val thr lys pro pro val ser) OPA

SEQ ID NOS: 821-822

FIGURE 46D

157/185

ORF according to Cole et al., 1998 (Nature 393: 537-544):
and containing the coding sequence Rv1411c:

1/1

31/11

SEQ ID NO: 823

tag ctc acc cag gtt gga ccg gtt cag tgt ctc gcc cat cac gtc gcc ggt gaa ttg gcc
AMB (leu thr gln val gly pro val gln cys leu gly his his val gly gly glu leu ala
61/21) SEQ ID NO: 824 91/31
gtc ggg caa tac atc gac gac cgt cag aca cac gcc gtt gac agc gat cga gtc gcc gtg
val gly gln tyr ile asp asp arg gln thr his ala val asp ser asp arg val ala val
121/41 151/51
gcc gcc gtc gcc ggt aac cat ccg acc gcg gat ggt cag ccg cgc cgc atc gac cag gcc
ala gly val gly gly asn his arg thr ala asp gly gln pro arg arg ile asp gln gly
181/61 211/71
ctc acg ccc ggt cac ttc tcc gcg ttc ctc aac aat tcc ggt gaa cat cgc acc agg tta
leu thr pro gly his phe ser ala phe leu asn asn ser gly glu his arg thr arg leu
241/81 271/91
ggc agc aat ccc gcg gac ccg cac ccc act cgc cga ccg gcc aac tca cag aca ccc tct
gly ser asn pro ala asp pro his pro thr arg arg pro ala asn ser gln thr pro ser
301/101 331/111
acg atg cag ggt atg ccg acc ccc aga cgc cac tgc cgt cgc atc gcc gtc ctc gcc gcc
thr met gln gly met arg thr pro arg arg his cys arg arg ile ala val leu ala ala
361/121 391/131
gtt agc atc gcc gcc act gtc gtt gcc gcc tgc tcg tcg gcc tcg aag cca agc gcc gga
val ser ile ala ala thr val val ala gly cys ser ser gly ser lys pro ser gly gly
421/141 451/151
cca ctt ccg gac gcg aag ccg ctg gtc gag gag gcc acc gcg cag acc aag gct ctc aag
pro leu pro asp ala lys pro leu val glu glu ala thr ala gln thr lys ala leu lys
481/161 511/171
agc gcg cac atg gtg ctg acg gtc aac gcc aag atc ccg gga ctg tct ctg aag acg ctg
ser ala his met val leu thr val asn gly lys ile pro gly leu ser leu lys thr leu
541/181 571/191
agc gcc gat ctc acc acc aac ccc acc gcc gcg acg gga aac gtc aag ctc acg ctg ggt
ser gly asp leu thr thr asn pro thr ala ala thr gly asn val lys leu thr leu gly
601/201 631/211
ggg tct gat atc gat gcc gac ttc gtg gtg ttc gac ggg atc ctg tac gcc acc ctg acg
gly ser asp ile asp ala asp phe val val phe asp gly ile leu tyr ala thr leu thr
661/221 691/231
ccc aac cag tgg agc gat ttc ggt ccc gcc gcc gac atc tac gac ccc gcc cag gtg ctg
pro asn gln trp ser asp phe gly pro ala ala asp ile tyr asp pro ala gln val leu
721/241 751/251
aat ccg gat acc gcc ctg gcc aac gtg ctg gcg aat ttc gcc gac gca aaa gcc gaa ggg
asn pro asp thr gly leu ala asn val leu ala asn phe ala asp ala lys ala glu gly
781/261 811/271
cgg gat acc atc aac gcc cag aac acc atc cgc atc agc ggg aag gta tcg gca cag gcg
arg asp thr ile asn gly gln asn thr ile arg ile ser gly lys val ser ala gln ala
841/281 871/291
gtg aac cag ata gcg ccg ccg ttc aac gcg acg cag ccg gtg ccg gcg acc gtc tgg att
val asn gln ile ala pro pro phe asn ala thr gln pro val pro ala thr val trp ile
901/301 931/311
cag gag acc gcc gat cat caa ctg gca cag gcc cag ttg gac cgc gcc tcg gcc aat tcc
gln glu thr gly asp his gln leu ala gln ala gln leu asp arg gly ser gly asn ser
961/321 991/331
gtc cag atg acc ttg tcg aaa tgg gcc gag aag gtc cag gtc acg aag ccc ccg gtg agc
val gln met thr leu ser lys trp gly glu lys val gln val thr lys pro pro val ser
1021/341
tga
OPA

SEQ ID NOS: 823-824

FIGURE 46E

1/1 31/11
 SEQ ID NO: 825 → gag ctg gtc aac ggc gcc ggc atc gac gac gcc gcc gtc gtg acc tgc cgg ccg gac agc
 glu leu val asn gly ala gly ile asp asp ala ala val val thr cys arg pro asp ser
 61/21 91/31
 SEQ ID NO: 826 → ctg gcc gat gcc cag cag atg gtc gag gcg gca ctg ggc cga tat ggc cgt ttg gac gga
 leu ala asp ala gln gln met val glu ala ala leu gly arg tyr gly arg leu asp gly
 121/41 151/51
 gtg ttg gtg gcc tcg ggc agc aac cat gtg gcg ccc att acc gag atg gcc gtc gag gac
 val leu val ala ser gly ser asn his val ala pro ile thr glu met ala val glu asp
 181/61 211/71
 ttc gac gct gtg atg gac gcg aac gtg cgg ggt gcc tgg ctg gtg tgt cgg gcg gcc gga
 phe asp ala val met asp ala asn val arg gly ala trp leu val cys arg ala ala gly
 241/81 271/91
 cgg gtg ctg ctc gag cag ggt cag ggc ggc agc gtg gtg ctg gtg tcg tcc gtt cgc ggc
 arg val leu leu glu gln gly gln gly gly ser val val leu val ser ser val arg gly
 301/101 331/111
 ggg ttg ggc aat gcc gcc ggt tac agc gcg tac tgc ccg tcg aag gcg ggc acc gat c
 gly leu gly asn ala ala gly tyr ser ala tyr cys pro ser lys ala gly thr asp

SEQ ID NOS: 825-826

FIGURE 47A

1/1 31/11
 SEQ ID NO: 827 → agc tgg tca acg gcg ccg gca tcg acg acg ccg ccg tcg tga cct gcc ggc cgg aca gcc
 (ser trp ser thr ala pro ala ser thr thr pro pro ser) OPA (pro ala gly arg thr ala
 61/21 91/31
 SEQ ID NO: 828 → tgg ccg atg ccc agc aga tgg tcg agg cgg cac tgg gcc gat atg gcc gtt tgg acg gag
 trp pro met pro ser arg trp ser arg arg his trp ala asp met ala val trp thr glu
 121/41 151/51
 tgt tgg tgg cct cgg gca gca acc atg tgg cgc cca tta ccg aga tgg ccg tcg agg act
 cys trp trp pro arg ala ala thr met trp arg pro leu pro arg trp pro ser arg thr
 181/61 211/71
 tcg acg ctg tga tgg acg cga acg tgc ggg gtg cct ggc tgg tgt gtc ggg cgg ccg gac
 ser thr leu) OPA (trp thr arg thr cys gly val pro gly trp cys val gly arg pro asp
 241/81 271/91
 SEQ ID NO: 830 → ggg tgc tgc tcg agc agg gtc agg gcg gca gcg tgg tgc tgg tgt cgt ccg ttc gcg gcg
 gly cys cys ser ser arg val arg ala ala ala trp cys trp cys arg pro phe ala ala
 301/101 331/111
 ggt tgg gca atg ccg ccg gtt aca gcg cgt act gcc cgt cga agg cgg gca ccg atc
 gly trp ala met pro pro val thr ala arg thr ala arg arg arg arg ala pro ile

SEQ ID NOS: 827-830

FIGURE 47B

1/1
 SEQ ID NO: 831 → gct ggt caa cgg cgc cgg cat cga cga cgc cgc cgt cgt gac ctg ccg gcc gga cag cct
 31/11
 SEQ ID NO: 832 → ala gly gln arg arg arg his arg arg arg arg arg arg asp leu pro ala gly gln pro
 91/31
 61/21
 ggc cga tgc cca gca gat ggt cga ggc ggc act ggg ccg ata tgg ccg ttt gga cgg agt
 gly arg cys pro ala asp gly arg gly gly thr gly pro ile trp pro phe gly arg ser
 151/51
 121/41
 gtt ggt ggc ctc ggg cag caa cca tgt ggc gcc cat tac cga gat ggc cgt cga gga ctt
 val gly gly leu gly gln gln pro cys gly ala his tyr arg asp gly arg arg gly leu
 211/71
 181/61
 cga cgc tgt gat gga cgc gaa cgt gcg ggg tgc ctg gct ggt gtg tcg ggc ggc cgg acg
 arg arg cys asp gly arg glu arg ala gly cys leu ala gly val ser gly gly arg thr
 271/91
 241/81
 ggt gct gct cga gca ggg tca ggg cgg cag cgt ggt gct ggt gtc gtc cgt tcg cgg cgg
 gly ala ala arg ala gly ser gly arg gln arg gly ala gly val val arg ser arg arg
 331/111
 301/101
 gtt ggg caa tgc cgc cgg tta cag cgc gta ctg ccc gtc gaa ggc ggg cac cga tc
 val gly gln cys arg arg leu gln arg val leu pro val glu gly gly his arg)

SEQ ID NOS: 831-832

FIGURE 47C

Coding sequence Rv1714 predicted by Cole et al., 1998 (Nature 393: 537-544) and containing seq 47A:

QID No: 833 → 1/1
 RIB No: 834 → 31/11

gtg gag gaa atg gcg ctg gct cag cag gtg ccg aac ctg ggt ctg gcg cgc ttc agc gtg
 val glu glu met ala leu ala gln gln val pro asn leu gly leu ala arg phe ser val
 61/21 91/31

cag gac aag tcg atc ctg atc acc ggc gcg acc ggt tcg ttg ggc cga gtt gcc gcc cgg
 gln asp lys ser ile leu ile thr gly ala thr gly ser leu gly arg val ala ala arg
 121/41 151/51

gcg ctg gcc gac gcg gga gcg cgg ctg aca ctg gcc ggc ggc aac tcg gcc ggt ctg gcc
 ala leu ala asp ala gly ala arg leu thr leu ala gly gly asn ser ala gly leu ala
 181/61 211/71

gag ctg gtc aac ggc gcc ggc atc gac gac gcc gcc gtc gtg acc tgc cgg ccg gac agc
 glu leu val asn gly ala gly ile asp asp ala ala val val thr cys arg pro asp ser
 241/81 271/91

ctg gcc gat gcc cag cag atg gtc gag gcg gca ctg ggc cga tat ggc cgt ttg gac gga
 leu ala asp ala gln gln met val glu ala ala leu gly arg tyr gly arg leu asp gly
 301/101 331/111

gtg ttg gtg gcc tcg ggc agc aac cat gtg gcg ccc att acc gag atg gcc gtc gag gac
 val leu val ala ser gly ser asn his val ala pro ile thr glu met ala val glu asp
 361/121 391/131

ttc gac gct gtg atg gac gcg aac gtg cgg ggt gcc tgg ctg gtg tgt cgg gcg gcc gga
 phe asp ala val met asp ala asn val arg gly ala trp leu val cys arg ala ala gly
 421/141 451/151

cgg gtg ctg ctc gag cag ggt cag ggc gcc agc gtg gtg ctg gtg tcg tcc gtt cgc gcc
 arg val leu leu glu gln gly gln gly gly ser val val leu val ser ser val arg gly
 481/161 511/171

ggg ttg ggc aat gcc gcc ggt tac agc gcg tac tgc ccg tcg aag gcg ggc acc gat ctg
 gly leu gly asn ala ala gly tyr ser ala tyr cys pro ser lys ala gly thr asp leu
 541/181 571/191

ttg gcc aag aca ttg gcg gcc gaa tgg ggc ggt cac gcc att cgg gtg aac gcg ctg gcg
 leu ala lys thr leu ala ala glu trp gly gly his gly ile arg val asn ala leu ala
 601/201 631/211

ccg acg gtg ttt cgg tcc gcg gtg acc gag tgg atg ttc acc gac gat ccg aag ggc cgg
 pro thr val phe arg ser ala val thr glu trp met phe thr asp asp pro lys gly arg
 661/221 691/231

gcc acc cgg gag gcg atg ctc gcc cgg atc ccg ttg cgc cgc ttc gcc gaa ccg gaa gac
 ala thr arg glu ala met leu ala arg ile pro leu arg arg phe ala glu pro glu asp
 721/241 751/251

ttc gtc ggc gcc ctg atc tat ctg ctc agc gac gcc tcg agc ttc tac acc ggc cag gtg
 phe val gly ala leu ile tyr leu leu ser asp ala ser ser phe tyr thr gly gln val
 781/261 811/271

atg tat ctg gac gcc ggg tac acc gca tgc tga
 met tyr leu asp gly gly tyr thr ala cys) OPA

SEQ ID NOS: 833-834

FIGURE 47D

ORF according to Cole et al., 1998 (Nature 393: 537-544) and containing the coding sequence Rv1714:

24/1	54/11
tag gtg gag gaa atg gcg ctg gct cag cag	gtg ccg aac ctg ggt ctg gcg cgc ttc agc
AMB (val glu glu met ala leu ala gln gln	val pro asn leu gly leu ala arg phe ser
84/21	114/31
gtg cag gac aag tcg atc ctg atc acc ggc	gcg acc ggt tcg ttg ggc cga gtt gcc gcc
val gln asp lys ser ile leu ile thr gly	ala thr gly ser leu gly arg val ala ala
144/41	174/51
cgg gcg ctg gcc gac gcg gga gcg cgg ctg	aca ctg gcc ggc ggc aac tcg gcc ggt ctg
arg ala leu ala asp ala gly ala arg leu	thr leu ala gly gly asn ser ala gly leu
204/61	234/71
gcc gag ctg gtc aac ggc gcc ggc atc gac	gac gcc gcc gtc gtg acc tgc cgg ccg gac
ala glu leu val asn gly ala gly ile asp	asp ala ala val val thr cys arg pro asp
264/81	294/91
agc ctg gcc gat gcc cag cag atg gtc gag	gcg gca ctg ggc cga tat ggc cgt ttg gac
ser leu ala asp ala gln gln met val glu	ala ala leu gly arg tyr gly arg leu asp
324/101	354/111
gga gtg ttg gtg gcc tcg ggc agc aac cat	gtg gcg ccc att acc gag atg gcc gtc gag
gly val leu val ala ser gly ser asn his	val ala pro ile thr glu met ala val glu
384/121	414/131
gac ttc gac gct gtg atg gac gcg aac gtg	cgg ggt gcc tgg ctg gtg tgt cgg gcg gcc
asp phe asp ala val met asp ala asn val	arg gly ala trp leu val cys arg ala ala
444/141	474/151
gga cgg gtg ctg ctc gag cag ggt cag ggc	ggc agc gtg gtg ctg gtg tcg tcc gtt cgc
gly arg val leu leu glu gln gly gln gly	gly ser val val leu val ser ser val arg
504/161	534/171
ggc ggg ttg ggc aat gcc gcc ggt tac agc	gcg tac tgc ccg tcg aag gcg ggc acc gat
gly gly leu gly asn ala ala gly tyr ser	ala tyr cys pro ser lys ala gly thr asp
564/181	594/191
ctg ttg gcc aag aca ttg gcg gcc gaa tgg	ggc ggt cac ggc att cgg gtg aac gcg ctg
leu leu ala lys thr leu ala ala glu trp	gly gly his gly ile arg val asn ala leu
624/201	654/211
gcg ccg acg gtg ttt cgg tcc gcg gtg acc	gag tgg atg ttc acc gac gat ccg aag ggc
ala pro thr val phe arg ser ala val thr	glu trp met phe thr asp asp pro lys gly
684/221	714/231
cgg gcc acc cgg gag gcg atg ctc gcc cgg	atc ccg ttg cgc cgc ttc gcc gaa ccg gaa
arg ala thr arg glu ala met leu ala arg	ile pro leu arg arg phe ala glu pro glu
744/241	774/251
gac ttc gtc ggc gcc ctg atc tat ctg ctc	agc gac gcc tcg agc ttc tac acc ggc cag
asp phe val gly ala leu ile tyr leu leu	ser asp ala ser ser phe tyr thr gly gln
804/261	834/271
gtg atg tat ctg gac ggc ggg tac acc gca	tgc tga
val met tyr leu asp gly gly tyr thr ala	cys) OPA

SEQ ID Nos. 835-836

FIGURE 47F

162/185

```
1/1 31/11
SEQ ID No. 837 agg ctc atg agc aag acg gtt ctc atc ctt ggc gcg ggt gtc ggc ggc ctg acc acc gcc
SEQ ID No. 838 arg leu met ser lys thr val leu ile leu gly ala gly val gly gly leu thr thr ala
61/21 91/31
gac acc ctc cgt caa ctg cta cca cct gag gat c
asp thr leu arg gln leu leu pro pro glu asp)
```

SEQ ID Nos 837-838

FIGURE 48A

```
1/1 31/11
SEQ ID No. 839 ggc tca tga gca aga cgg ttc tca tcc ttg gcg cgg gtg tgc gcg gcc tga cca ccg ccg
gly ser OPA(ala arg arg phe ser ser leu ala arg val ser ala ala)OPA(pro pro pro
61/21 SEQ ID No. 840 91/31 SEQ ID No. 841
aca ccc tcc gtc aac tgc tac cac ctg agg atc
thr pro ser val asn cys tyr his leu arg ile)
```

SEQ ID Nos. 839-841

FIGURE 48B

```
1/1 31/11
SEQ ID No. 842 gct cat gag caa gac ggt tct cat cct tgg cgc ggg tgt cgg cgg cct gac cac cgc cga
SEQ ID No. 843 ala his glu gln asp gly ser his pro trp arg gly cys arg arg pro asp his arg arg
61/21
cac cct ccg tca act gct acc acc tga gga tc
his pro pro ser thr ala thr thr)OPA gly
```

SEQ ID Nos. 842-843

FIGURE 48C

Coding sequence Rv0331 predicted by Cole et al., 1998 (Nature 393: 537-544) and containing seq48A:

1/1
 31/11
 320 ID No. 844 atg agc aag acg gtt ctc atc ctt ggc gcg ggt gtc ggc ggc ctg acc acc gcc gac acc
 320 ID No. 845 (Met ser lys thr val leu ile leu gly ala gly val gly gly leu thr thr ala asp thr
 61/21 91/31
 ctc cgt caa ctg cta cca cct gag gat cga atc ata ttg gtg gac agg agc ttt gac ggg
 leu arg gln leu leu pro pro glu asp arg ile ile leu val asp arg ser phe asp gly
 121/41 151/51
 acg ctg ggc ttg tct ttg cta tgg gtg ttg cgg ggc tgg cgg cgg cct gac gac gtc cgc
 thr leu gly leu ser leu leu trp val leu arg gly trp arg arg pro asp asp val arg
 181/61 211/71
 gtc cgc ccc acc gcg gcg tct ctg ccc ggt gtg gaa atg gtt act gca acc gtc gcc cac
 val arg pro thr ala ala ser leu pro gly val glu met val thr ala thr val ala his
 241/81 271/91
 att gac atc gcg gcc cag gta gtg cac acc gac aac agc gtc atc ggc tat gac gcg ttg
 ile asp ile ala ala gln val val his thr asp asn ser val ile gly tyr asp ala leu
 301/101 331/111
 gtg atc gca tta ggt gcg gcg ctg aac acc gac gcc gtt ccc gga ctg tct gac gcg ctc
 val ile ala leu gly ala ala leu asn thr asp ala val pro gly leu ser asp ala leu
 361/121 391/131
 gac gcc gac gtc gcg ggc cag ttc tac acc ctg gac ggc gcg gct gag ctg cgt gcg aag
 asp ala asp val ala gly gln phe tyr thr leu asp gly ala ala glu leu arg ala lys
 421/141 451/151
 gtc gag gcg ctc gag cat ggc cgg atc gct gtg gct atc gcc ggg gtg cgg ttc aaa tgc
 val glu ala leu glu his gly arg ile ala val ala ile ala gly val pro phe lys cys
 481/161 511/171
 cca gcc gca ccg ttc gaa gcg gcg ttt ctg atc gcc gcc caa ctc ggt gac cgc tac gcc
 pro ala ala pro phe glu ala ala phe leu ile ala ala gln leu gly asp arg tyr ala
 541/181 571/191
 acc gga acc gta cag atc gac acg ttc acg cct gac ccg ctg ccg atg ccc gtt gca ggt
 thr gly thr val gln ile asp thr phe thr pro asp pro leu pro met pro val ala gly
 601/201 631/211
 ccc gag gtc ggc gag gct ttg gtc tct atg ctc aag gat cac ggt gtc ggc ttc cat cct
 pro glu val gly glu ala leu val ser met leu lys asp his gly val gly phe his pro
 661/221 691/231
 cgc aag gcc cta gct cgc gtc gat gag gcc gca agg acg atg cac ttc ggt gac ggc acg
 arg lys ala leu ala arg val asp glu ala ala arg thr met his phe gly asp gly thr
 721/241 751/251
 tcc gaa ccg ttc gat ctg ctt gcc gtg gtc ccc ccg cac gtg ccc tcc gcc gcg gcg cgg
 ser glu pro phe asp leu leu ala val val pro pro his val pro ser ala ala ala arg
 781/261 811/271
 tca gcg ggt ctc agc gaa tcc ggg tgg ata ccc gtg gac ccg cgc acc ctg tcc act agc
 ser ala gly leu ser glu ser gly trp ile pro val asp pro arg thr leu ser thr ser
 841/281 871/291
 gcc gac aac gtg tgg gcc atc ggc gat gcg acc gtg ctg acg ctg ccg aat ggc aaa ccg
 ala asp asn val trp ala ile gly asp ala thr val leu thr leu pro asn gly lys pro
 901/301 931/311
 ctg ccc aag gct gcc gtg ttc gcc gaa gcc cag gcc gca gtt gtc gcc cac ggc gtc gcc
 leu pro lys ala ala val phe ala glu ala gln ala ala val val ala his gly val ala
 961/321 991/331
 cgc cat ctc ggt tac gac gta gct gag cgc cac ttc acc ggc acg ggc gcc tgc tac gtc
 arg his leu gly tyr asp val ala glu arg his phe thr gly thr gly ala cys tyr val
 1021/341 1051/351
 gag acc ggt gat cac cag gca gcc aag ggc gac gcc gat ttc ttc gct ccg tct gcg ccc
 glu thr gly asp his gln ala ala lys gly asp gly asp phe phe ala pro ser ala pro
 1081/361 1111/371
 tct gtg acg ctg tac ccg ccg tct cgg gag ttt cac gag gag aag gtc gca caa gaa ctg
 ser val thr leu tyr pro pro ser arg glu phe his glu glu lys val ala gln glu leu
 1141/381
 gcc tgg ctg acc cgc tgg aag acg tga
 ala trp leu thr arg trp lys thr)OPA

ORF according to Cole et al., 1998 (Nature 393: 537-544) and containing coding sequence Rv0331:

1/1	31/11
EO ID No. 846	tga aca ccc gcg ccg acg cgg cga caa tcg cgg aaa acc ggt ccg cgg gaa tgc tgc ggg
EO ID No. 847	OPA thr pro ala pro thr arg arg gln ser arg lys thr gly pro arg glu cys cys gly
61/21	91/31
cca tgg gcc gat aat agt ttg act gac tcg gtc agt cac ccc aag acc ttg cgc aag act	
pro trp ala asp asn ser leu thr asp ser	val ser his pro lys thr leu arg lys thr
121/41	151/51
gcg gcg gaa tct aat att cca aag ata tat gga act cga tgc gaa gga atc agg ctc atg	
ala ala glu ser asn ile pro lys ile tyr gly thr arg cys glu gly ile arg leu met	
181/61	211/71
agc aag acg gtt ctc atc ctt ggc gcg ggt gtc ggc ggc ctg acc acc gcc gac acc ctc	
ser lys thr val leu ile leu gly ala gly val gly gly leu thr thr ala asp thr leu	
241/81	271/91
cgt caa ctg cta cca cct gag gat cga atc ata ttg gtg gac agg agc ttt gac ggg acg	
arg gln leu leu pro pro glu asp arg ile ile leu val asp arg ser phe asp gly thr	
301/101	331/111
ctg ggc ttg tcg ttg cta tgg gtg ttg cgg ggc tgg cgg cgg cct gac gac gtc cgc gtc	
leu gly leu ser leu leu trp val leu arg gly trp arg arg pro asp asp val arg val	
361/121	391/131
gcg ccc acc gcg gcg tcg ctg ccc ggt gtg gaa atg gtt act gca acc gtc gcc cac att	
arg pro thr ala ala ser leu pro gly val glu met val thr ala thr val ala his ile	
421/141	451/151
gac atc gcg gcc cag gta gtg cac acc gac aac agc gtc atc ggc tat gac gcg ttg gtg	
asp ile ala ala gln val val his thr asp asn ser val ile gly tyr asp ala leu val	
481/161	511/171
atc gca tta ggt gcg gcg ctg aac acc gac gcc gtt ccc gga ctg tcg gac gcg ctc gac	
ile ala leu gly ala ala leu asn thr asp ala val pro gly leu ser asp ala leu asp	
541/181	571/191
gcc gac gtc gcg ggc cag ttc tac acc ctg gac ggc gcg gct gag ctg cgt gcg aag gtc	
ala asp val ala gly gln phe tyr thr leu asp gly ala ala glu leu arg ala lys val	
601/201	631/211
gag gcg ctc gag cat ggc cgg atc gct gtg gct atc gcc ggg gtg ccg ttc aaa tgc cca	
glu ala leu glu his gly arg ile ala val ala ile ala gly val pro phe lys cys pro	
661/221	691/231
gcc gca ccg ttc gaa gcg gcg ttt ctg atc gcc gcc caa ctc ggt gac cgc tac gcc acc	
ala ala pro phe glu ala ala phe leu ile ala ala gln leu gly asp arg tyr ala thr	
721/241	751/251
gga acc gta cag atc gac acg ttc acg cct gac ccg ctg ccg atg ccc gtt gca ggt ccc	
gly thr val gln ile asp thr phe thr pro asp pro leu pro met pro val ala gly pro	
781/261	811/271
gag gtc ggc gag gct ttg gtc tcg atg ctc aag gat cac ggt gtc ggc ttc cat cct cgc	
glu val gly glu ala leu val ser met leu lys asp his gly val gly phe his pro arg	
841/281	871/291
aag gcc cta gct cgc gtc gat gag gcc gca agg acg atg cac ttc ggt gac ggc acg tcc	
lys ala leu ala arg val asp glu ala ala arg thr met his phe gly asp gly thr ser	

SEQ ID Nos. 846-847

FIGURE 48E

901/301	931/311
gaa ccg ttc gat ctg ctt gcc gtg gtc ccc	ccg cac gtg ccc tcc gcc gcg gcg cgg tca
glu pro phe asp leu leu ala val val pro	pro his val pro ser ala ala ala arg ser
961/321	991/331
gcg ggt ctc agc gaa tcc ggg tgg ata ccc	gtg gac ccg cgc acc ctg tcc act agc gcc
ala gly leu ser glu ser gly trp ile pro	val asp pro arg thr leu ser thr ser ala
1021/341	1051/351
gac aac gtg tgg gcc atc ggc gat gcg acc	gtg ctg acg ctg ccg aat ggc aaa ccg ctg
asp asn val trp ala ile gly asp ala thr	val leu thr leu pro asn gly lys pro leu
1081/361	1111/371
ccc aag gct gcc gtg ttc gcc gaa gcc cag	gcc gca gtt gtc gcc cac ggc gtc gcc cgc
pro lys ala ala val phe ala glu ala gln	ala ala val val ala his gly val ala arg
1141/381	1171/391
cat ctc ggt tac gac gta gct gag cgc cac	ttc acc ggc acg ggc gcc tgc tac gtc gag
his leu gly tyr asp val ala glu arg his	phe thr gly thr gly ala cys tyr val glu
1201/401	1231/411
acc ggt gat cac cag gca gcc aag ggc gac	ggc gat ttc ttc gct ccg tgc gcg ccc tgc
thr gly asp his gln ala ala lys gly asp	gly asp phe phe ala pro ser ala pro ser
1261/421	1291/431
gtg acg ctg tac ccg ccg tgc cgg gag ttt	cac gag gag aag gtc gca caa gaa ctg gcc
val thr leu tyr pro pro ser arg glu phe	his glu glu lys val ala gln glu leu ala
1321/441	
tgg ctg acc cgc tgg aag acg tga	
trp leu thr arg trp lys thr)OPA	

SEQ ID Nos. 846-847(continued)

FIGURE 48E (continued)

Fragment amplified by PCR based on the sequence similarities with a serine protease of the E.coli htrA family (creation of the BamHI site at the 5' end and of the SnaBI site at the 3' end) and subcloned into the vector pJVED:

```

1/1
SEQ ID NO. 848 cca tct aca ccg ctc aac agc cgg gcc aga cgc tgc cgg tcg gtg ctg ccg aga agg cgg
SEQ ID NO. 849 pro ser thr pro leu asn ser arg ala arg arg cys arg ser val leu pro arg arg arg)
61/21
tga tcc gtg gcg agt tgt tca tgt cgc ggc gca cca ccg ccg acc aac ggg tgc ttg cca
OPA (ser val ala ser cys ser cys arg gly ala pro pro pro thr asn gly cys leu pro
121/41
tcc gtc tga cca acg gta gtt cgc tgc tga tct cca aaa gtc tca agc cca ccg aag cag
ser val) OPA (pro thr val val arg cys) OPA (ser pro lys val ser ser pro pro lys gln
181/61 SEQ ID NO. 851
tca tga aca agc tgc gtt ggg tgc tat tga tcg tgg gtg gga tcg ggg tgg ccg tcg ccg
ser) OPA (thr ser cys val gly cys tyr) OPA (ser trp val gly ser gly trp arg ser pro
241/81 SEQ ID NO. 853
cgg tgg ccg ggg gga tgg tca ccc ggg ccg ggc tga ggc ccg tgg gcc gcc tca ccg aag
arg trp pro gly gly trp ser pro gly pro gly) OPA (gly arg trp ala ala ser pro lys
301/101
cgg ccg agc ggg tgg cgc gaa ccg acg acc tgc ggc cca tcc ccg tct tcg gca gcg acg
arg pro ser gly trp arg glu pro thr thr cys gly pro ser pro ser ser ala ala thr
361/121
aat tgg cca ggc tga cag agg cat tca att taa tgc tgc ggg cgc tgg ccg agt cac ggg
asn trp pro gly) OPA (gln arg his ser ile) OCH (cys cys gly arg trp pro ser his gly
421/141
aac ggc agg caa ggc tgg tta ccg acg ccg gac atg aat tgc gta ccc cgc taa cgt cgc
asn gly arg gln gly trp leu pro thr pro asp met asn cys val pro arg) OCH (arg arg
481/161
tgc gca cca atg tcg aac tct tga tgg cct cga tgg ccc ccg ggg ctc cgc ggc tac cca
cys ala pro met ser asn ser) OPA (trp pro arg trp pro arg gly leu arg gly tyr pro
541/181
agc agg aga tgg tcg acc tgc gtg ccg atg tgc tgg ctc aaa tcg agg aat tgt cca cac
ser arg arg trp ser thr cys val pro met cys trp leu lys ser arg asn cys pro his
601/201
tgg tag gcg att tgg tgg acc tgt ccc gag gcg acg ccg gag aag tgg tgc acg agc ccg
trp) AMB (ala ile trp trp thr cys pro glu ala thr pro glu lys trp cys thr ser arg
661/221 SEQ ID NO. 860
tcg aca tgg ctg acg tcg tcg acc gca gcc tgg agc ggg tca ggc ggc ggc gca acg ata
ser thr trp leu thr ser ser thr ala ala trp ser gly ser gly gly ala thr ile
721/241
tcc ttt tcg acg tcg agg tga ttg ggt ggc agg ttt atg gcg ata ccg ctg gat tgt cgc
ser phe ser thr ser arg) OPA (leu gly gly arg phe met ala ile pro leu asp cys arg
781/261
gga tgg cgc tta acc tga tgg tga aca acg ccg cga agt gga gcc cgc ccg gcg gcc acg tgg
gly trp arg leu thr) OPA (trp thr thr pro arg ser gly ala arg arg ala ala thr trp
841/281
gtg tca ggc tga gcc agc tcg acg cgt cgc acg ctg agc tgg tgg ttt ccg acc gcg gcc
val ser gly) OPA (ala ser ser thr arg arg thr leu ser trp trp phe pro thr ala ala
SEQ ID NO. 863

```

SEQ ID NOS 848-863

FIGURE 49A

901/301	931/311
cgg gca ttc ccg tgc agg agc gcc gtc tgg	tgt ttg aac ggt ttt acc ggt cgg cat cgg
arg ala phe pro cys arg ser ala val trp	cys leu asn gly phe thr gly arg his arg
961/321	991/331
cac ggg cgt tgc cgg gtt cgg gcc tcg ggt	tgg cga tcg tca aac agg tgg tgc tca acc
his gly arg cys arg val arg ala ser gly	trp arg ser ser asn arg trp cys ser thr
1021/341	1051/351
acg gcg gat tgc tgc gca tcg aag aca ccg	acc cag gcg gcc agc ccc ctg gaa cgt cga
thr ala asp cys cys ala ser lys thr pro	thr gln ala ala ser pro leu glu arg arg
1081/361	1111/371
ttt acg tgc tgc tcc ccg gcc gtc gga tgc	cga ttc cgc agc ttc ccg gtg cga cgg ctg
phe thr cys cys ser pro ala val gly cys	arg phe arg ser phe pro val arg arg leu
1141/381	1171/391
gcg ctc gga gca cgg aca tcg aga act ctc	ggg gtt cgg cga acg tta tct cag tgg aat
ala leu gly ala arg thr ser arg thr leu	gly val arg arg thr leu ser gln trp asn
1201/401	1231/411
ctc agt cca cgc gcg caa cct agt tgt gca	gtt act gtt gaa agc cac acc cat gcc agt
leu ser pro arg ala gln pro ser cys ala	val thr val glu ser his thr his ala ser
1261/421	1291/431
cca cgc atg gcc aag ttg gcc cga gta gtg	ggc cta gta cag gaa gag caa cct agc gac
pro arg met ala lys leu ala arg val val	gly leu val gln glu glu gln pro ser asp
1321/441	1351/451
atg acg aat cac cca cgg tat tcg cca ccg	ccg cag cag ccg gga acc cca ggt tat gct
met thr asn his pro arg tyr ser pro pro	pro gln gln pro gly thr pro gly tyr ala
1381/461	1411/471
cag ggg cag cag caa acg tac agc cag cag	ttc gac tgg cgt tac cca ccg tcc ccg ccc
gln gly gln gln gln thr tyr ser gln gln	phe asp trp arg tyr pro pro ser pro pro
1441/481	1471/491
ccg cag cca acc cag tac cgt caa ccc tac	gag gcg ttg ggt ggt acc ccg ccg ggt ctg
pro gln pro thr gln tyr arg gln pro tyr	glu ala leu gly gly thr arg pro gly leu
1501/501	1531/511
ata cct ggc gtg att ccg acc atg acg ccc	cct cct ggg atg gtt cgc caa cgc cct cgt
ile pro gly val ile pro thr met thr pro	pro pro gly met val arg gln arg pro arg
1561/521	1591/531
gca ggc atg ttg gcc atc ggc gcg gtg acg	ata gcg gtg gtg tcc gcc ggc atc ggc ggc
ala gly met leu ala ile gly ala val thr	ile ala val val ser ala gly ile gly gly
1621/541	1651/551
gcg gcc gca tcc ctg gtc ggg ttc aac ccg	gca ccc gcc ggc ccc agc ggc ggc cca gtg
ala ala ala ser leu val gly phe asn arg	ala pro ala gly pro ser gly gly pro val
1681/561	1711/571
gct gcc agc gcg gcg cca agc atc ccc gca	gca aac atg ccg ccg ggg tcg gtc gaa cag
ala ala ser ala ala pro ser ile pro ala	ala asn met pro pro gly ser val glu gln
1741/581	1771/591
gtg gcg gcc aag gtg gtg ccc agt gtc gtc	atg ttg gaa acc gat ctg ggc cgc cag tcg
val ala ala lys val val pro ser val val	met leu glu thr asp leu gly arg gln ser
1801/601	1831/611
gag gag ggc tcc ggc atc att ctg tct gcc	gag ggg ctg atc ttg acc aac aac cac gtg
glu glu gly ser gly ile ile leu ser ala	glu gly leu ile leu thr asn asn his val
1861/621	1891/631
atc gcg gcg gcc gcc aag cct ccc ctg ggc	agt ccg ccg ccg aaa acg acg gta
ile ala ala ala ala lys pro pro leu gly	ser pro pro pro lys thr thr val)

SEQ ID Nos. 848-862 continued 1)

FIGURE 49A (continued 1)

1/1

31/11

ID NO. 864 cat cta cac cgc tca aca gcc ggg cca gac gct gcc ggt cgg tgc tgc cga gaa ggc ggt
 SEQ ID NO. 865 his leu his arg ser thr ala gly pro asp ala ala gly arg cys cys arg glu gly gly
 61/21 91/31
 gat ccg tgg cga gtt gtt cat gtc gcg gcg cac cac cgc cga cca acg ggt gct tgc cat
 asp pro trp arg val val his val ala ala his his arg arg pro thr gly ala cys his
 121/41 151/51
 ccg tct gac caa cgg tag ttc gct gct gat ctc caa aag tct caa gcc cac cga agc agt
 pro ser asp gln arg) AMB (phe ala ala asp leu gln lys ser gln ala his arg ser ser
 181/61 211/71
 cat gaa caa gct gcg ttg ggt gct att gat cgt ggg tgg gat cgg ggt ggc ggt cgc cgc
 his glu gln ala ala leu gly ala ile asp arg gly trp asp arg gly gly gly arg arg
 241/81 271/91
 ggt ggc cgg ggg gat ggt cac ccg ggc cgg gct gag gcc ggt ggg ccg cct cac cga agc
 gly gly arg gly asp gly his pro gly arg ala glu ala gly gly pro pro his arg ser
 301/101 331/111
 ggc cga gcg ggt ggc gcg aac cga cga cct gcg gcc cat ccc cgt ctt cgg cag cga cga
 gly arg ala gly gly ala asn arg arg pro ala ala his pro arg leu arg gln arg arg
 361/121 391/131
 att ggc cag gct gac aga ggc att caa ttt aat gct gcg ggc gct ggc cga gtc acg gga
 ile gly gln ala asp arg gly ile gln phe asn ala ala gly ala gly arg val thr gly
 421/141 451/151
 acg gca ggc aag gct ggt tac cga cgc cgg aca tga att gcg tac ccc gct aac gtc gct
 thr ala gly lys ala gly tyr arg arg arg thr) OPA (ile ala tyr pro ala asn val ala
 481/161 511/171
 gcg cac caa tgt cga act ctt gat ggc ctc gat ggc ccc ggg ggc tcc gcg gct acc caa
 ala his gln cys arg thr leu asp gly leu asp gly pro gly gly ser ala ala thr gln
 541/181 571/191
 gca gga gat ggt cga cct gcg tgc cga tgt gct ggc tca aat cga gga att gtc cac act
 ala gly asp gly arg pro ala cys arg cys ala gly ser asn arg gly ile val his thr
 601/201 631/211
 ggt agg cga ttt ggt gga cct gtc ccg agg cga cgc cgg aga agt ggt gca cga gcc ggt
 gly arg arg phe gly gly pro val pro arg arg arg arg arg ser gly ala arg ala gly
 661/221 691/231
 cga cat ggc tga cgt cgt cga ccg cag cct gga gcg ggt cag gcg gcg gcg caa cga tat
 arg his gly) OPA (arg arg arg pro gln pro gly ala gly gln ala ala ala gln arg tyr
 721/241 751/251
 cct ttt cga cgt cga ggt gat tgg gtg gca ggt tta tgg cga tac cgc tgg att gtc gcg
 pro phe arg arg arg gly asp trp val ala gly leu trp arg tyr arg trp ile val ala
 781/261 811/271
 gat ggc gct taa cct gat gga caa cgc cgc gaa gtg gag ccc gcc ggg cgg cca cgt ggg
 asp gly ala) OCH (pro asp gly gln arg arg glu val glu pro ala gly arg pro arg gly
 841/281 871/291
 tgt cag gct gag cca gct cga cgc gtc gca cgc tga gct ggt ggt ttc cga ccg cgg ccc
 cys gln ala glu pro ala arg arg val ala arg) OPA (ala gly gly phe arg pro arg pro
 901/301 931/311
 ggg cat tcc cgt gca gga gcg ccg tct ggt gtt tga acg gtt tta ccg gtc ggc atc ggc
 gly his ser arg ala gly ala pro ser gly val) OPA (thr val leu pro val gly ile gly
 961/321 991/331
 acg ggc gtt gcc ggg ttc ggg cct cgg gtt ggc gat cgt caa aca ggt ggt gct caa cca
 thr gly val ala gly phe gly pro arg val gly asp arg gln thr gly gly ala gln pro
 1021/341 1051/351
 cgg cgg att gct gcg cat cga aga cac cga ccc agg cgg cca gcc ccc tgg aac gtc gat
 arg arg ile ala ala his arg arg his arg pro arg arg pro ala pro trp asn val asp

1081/361
 tta cgt gct gct ccc cgg ccg tcg gat gcc gat tcc gca gct tcc cgg tgc gac ggc tgg
 leu arg ala ala pro arg pro ser asp ala asp ser ala ala ser arg cys asp gly trp
 1141/381
 cgc tcg gag cac gga cat cga gaa ctc tcg ggg ttc ggc gaa cgt tat ctc agt gga atc
 arg ser glu his gly his arg glu leu ser gly phe gly glu arg tyr leu ser gly ile
 1201/401
 tca gtc cac gcg cgc aac cta gtt gtg cag tta ctg ttg aaa gcc aca ccc atg cca gtc
 ser val his ala arg asn leu val val gln leu leu leu lys ala thr pro met pro val
 1261/421
 cac gca tgg cca agt tgg ccc gag tag tgg gcc tag tac agg aag agc aac cta gcg aca
 his ala trp pro ser trp pro glu)AMB trp ala AMB (tyr arg lys ser asn leu ala thr)
 1321/441
 tga cga atc acc cac ggt att cgc cac cgc cgc agc agc cgg gaa ccc cag gtt atg ctc
 OPA (arg ile thr his gly ile arg his arg arg ser ser arg glu pro gln val met leu
 1381/461
 agg ggc agc agc aaa cgt aca gcc agc agt tcg act ggc gtt acc cac cgt ccc cgc ccc
 arg gly ser ser lys arg thr ala ser ser ser thr gly val thr his arg pro arg pro
 1441/481
 cgc agc caa ccc agt acc gtc aac cct acg agg cgt tgg gtg gta ccc ggc cgg gtc tga
 arg ser gln pro ser thr val asn pro thr arg arg trp val val pro gly arg val) OPA
 1501/501
 tac ctg gcg tga ttc cga cca tga cgc ccc ctc ctg gga tgg ttc gcc aac gcc ctc gtg
 tyr leu ala OPA phe arg pro OPA (arg pro leu leu gly trp phe ala asn ala leu val
 1561/521
 cag gca tgt tgg cca tcg gcg cgg tga cga tag cgg tgg tgt ccg ccg gca tcg gcg gcg
 gln ala cys trp pro ser ala arg) OPA arg AMB (arg trp cys pro pro ala ser ala ala
 1621/541
 cgg ccg cat ccc tgg tcg ggt tca acc ggg cac ccg ccg gcc cca gcg gcg gcc cag tgg
 arg pro his pro trp ser gly ser thr gly his pro pro ala pro ala ala ala gln trp
 1681/561
 ctg cca gcg cgg cgc caa gca tcc ccg cag caa aca tgc cgc cgg ggt cgg tcg aac agg
 leu pro ala arg arg gln ala ser pro gln gln thr cys arg arg gly arg ser asn arg
 1741/581
 tgg cgg cca agg tgg tgc cca gtg tcg tca tgt tgg aaa ccg atc tgg gcc gcc agt cgg
 trp arg pro arg trp cys pro val ser ser cys trp lys pro ile trp ala ala ser arg
 1801/601
 agg agg gct ccg gca tca ttc tgt ctg ccg agg ggc tga tct tga cca aca acc acg tga
 arg arg ala pro ala ser phe cys leu pro arg gly) OPA ser OPA (pro thr thr thr) OPA
 1861/621
 tcg cgg cgg ccg cca agc ctc ccc tgg gca gtc cgc cgc cga aaa cga cgg ta
 (ser arg arg pro pro ser leu pro trp ala val arg arg arg lys arg arg)
 SEQ ID NO. 877

SEQ ID NO. 874-877 (continued 1)

FIGURE 49B (continued 1)

1/1

31/11

SEQ ID NO. 878 atc tac acc gct caa cag ccg ggc cag acg ctg ccg gtc ggt gct gcc gag aag gcg gtg
 SEQ ID NO. 879 ile tyr thr ala gln gln pro gly gln thr leu pro val gly ala ala glu lys ala val
 61/21 91/31
 atc cgt ggc gag ttg ttc atg tcg cgg cgc acc acc gcc gac caa cgg gtg ctt gcc atc
 ile arg gly glu leu phe met ser arg arg thr thr ala asp gln arg val leu ala ile
 121/41 151/51
 cgt ctg acc aac ggt agt tcg ctg ctg atc tcc aaa agt ctc aag ccc acc gaa gca gtc
 arg leu thr asn gly ser ser leu leu ile ser lys ser leu lys pro thr glu ala val
 181/61 211/71
 atg aac aag ctg cgt tgg gtg cta ttg atc gtg ggt ggg atc ggg gtg gcg gtc gcc gcg
 met asn lys leu arg trp val leu leu ile val gly gly ile gly val ala val ala ala
 241/81 271/91
 gtg gcc ggg ggg atg gtc acc cgg gcc ggg ctg agg ccg gtg ggc cgc ctc acc gaa gcg
 val ala gly gly met val thr arg ala gly leu arg pro val gly arg leu thr glu ala
 301/101 331/111
 gcc gag cgg gtg gcg cga acc gac gac ctg cgg ccc atc ccc gtc ttc ggc agc gac gaa
 ala glu arg val ala arg thr asp asp leu arg pro ile pro val phe gly ser asp glu
 361/121 391/131
 ttg gcc agg ctg aca gag gca ttc aat tta atg ctg cgg gcg ctg gcc gag tca cgg gaa
 leu ala arg leu thr glu ala phe asn leu met leu arg ala leu ala glu ser arg glu
 421/141 451/151
 cgg cag gca agg ctg gtt acc gac gcc gga cat gaa ttg cgt acc ccg cta acg tcg ctg
 arg gln ala arg leu val thr asp ala gly his glu leu arg thr pro leu thr ser leu
 481/161 511/171
 cgc acc aat gtc gaa ctc ttg atg gcc tcg atg gcc ccg ggg gct ccg cgg cta ccc aag
 arg thr asn val glu leu leu met ala ser met ala pro gly ala pro arg leu pro lys
 541/181 571/191
 cag gag atg gtc gac ctg cgt gcc gat gtg ctg gct caa atc gag gaa ttg tcc aca ctg
 gln glu met val asp leu arg ala asp val leu ala gln ile glu glu leu ser thr leu
 601/201 631/211
 gta gcc gat ttg gtg gac ctg tcc cga ggc gac gcc gga gaa gtg gtg cac gag ccg gtc
 val gly asp leu val asp leu ser arg gly asp ala gly glu val val his glu pro val
 661/221 691/231
 gac atg gct gac gtc gtc gac cgc agc ctg gag cgg gtc agg cgg cgg cgc aac gat atc
 asp met ala asp val val asp arg ser leu glu arg val arg arg arg arg asn asp ile
 721/241 751/251
 ctt ttc gac gtc gag gtg att ggg tgg cag gtt tat ggc gat acc gct gga ttg tcg cgg
 leu phe asp val glu val ile gly trp gln val tyr gly asp thr ala gly leu ser arg
 781/261 811/271
 atg gcg ctt aac ctg atg gac aac gcc gcg aag tgg agc ccg ccg ggc ggc cac gtg ggt
 met ala leu asn leu met asp asn ala ala lys trp ser pro pro gly gly his val gly
 841/281 871/291
 gtc agg ctg agc cag ctc gac gcg tcg cac gct gag ctg gtg gtt tcc gac cgc ggc ccg
 val arg leu ser gln leu asp ala ser his ala glu leu val val ser asp arg gly pro
 901/301 931/311
 ggc att ccc gtg cag gag cgc cgt ctg gtg ttt gaa cgg ttt tac cgg tcg gca tcg gca
 gly ile pro val gln glu arg arg leu val phe glu arg phe tyr arg ser ala ser ala
 961/321 991/331
 cgg gcg ttg ccg ggt tcg ggc ctc ggg ttg gcg atc gtc aaa cag gtg gtg ctc aac cac
 arg ala leu pro gly ser gly leu gly leu ala ile val lys gln val val leu asn his

1021/341
 ggc gga ttg ctg cgc atc gaa gac acc gac cca ggc ggc cag ccc cct gga acg tcg att
 gly gly leu leu arg ile glu asp thr asp pro gly gly gln pro pro gly thr ser ile
 1081/361
 tac gtg ctg ctc ccc ggc cgt cgg atg ccg att ccg cag ctt ccc ggt ggc acg gct ggc
 tyr val leu leu pro gly arg arg met pro ile pro gln leu pro gly ala thr ala gly
 1141/381
 gct cgg agc acg gac atc gag aac tct cgg ggt tcg ggc aac gtt atc tca gtg gaa tct
 ala arg ser thr asp ile glu asn ser arg gly ser ala asn val ile ser val glu ser
 1201/401
 cag tcc acg cgc gca acc tag ttg tgc agt tac tgt tga aag cca cac cca tgc cag tcc
 gln ser thr arg ala thr)AMB (leu cys ser tyr cys)OPA (lys pro his pro cys gln ser
 1261/421
 acg cat ggc caa gtt ggc ccg agt agt ggg cct agt aca gga aga gca acc tag cga cat
 thr his gly gln val gly pro ser ser gly pro ser thr gly arg ala thr)AMB (arg his
 1321/441
 gac gaa tca ccc acg gta ttc gcc acc gcc gca gca gcc ggg aac ccc agg tta tgc tca
 asp glu ser pro thr val phe ala thr ala ala ala ala gly asn pro arg leu cys ser
 1381/461
 ggg gca gca gca aac gta cag cca gca gtt cga ctg ggc tta ccc acc gtc ccc gcc ccc
 gly ala ala ala asn val gln pro ala val arg leu ala leu pro thr val pro ala pro
 1441/481
 gca gcc aac cca gta ccg tca acc cta cga ggc gtt ggg tgg tac ccg gcc ggg tct gat
 ala ala asn pro val pro ser thr leu arg gly val gly trp tyr pro ala gly ser asp
 1501/501
 acc tgg cgt gat tcc gac cat gac gcc ccc tcc tgg gat ggt tcg cca acg ccc tcg tgc
 thr trp arg asp ser asp his asp ala pro ser trp asp gly ser pro thr pro ser cys
 1561/521
 agg cat gtt ggc cat cgg cgc ggt gac gat agc ggt ggt gtc cgc cgg cat cgg cgg cgc
 arg his val gly his arg arg gly asp asp ser gly gly val arg arg his arg arg arg
 1621/541
 ggc cgc atc cct ggt cgg gtt caa ccg ggc acc cgc cgg ccc cag cgg cgg ccc agt ggc
 gly arg ile pro gly arg val gln pro gly thr arg arg pro gln arg arg pro ser gly
 1681/561
 tgc cag cgc ggc gcc aag cat ccc cgc agc aaa cat gcc gcc ggg gtc ggt cga aca ggt
 cys gln arg gly ala lys his pro arg ser lys his ala ala gly val gly arg thr gly
 1741/581
 ggc ggc caa ggt ggt gcc cag tgt cgt cat gtt gga aac cga tct ggg ccg cca gtc gga
 gly gly gln gly gly ala gln cys arg his val gly asn arg ser gly pro pro val gly
 1801/601
 gga ggg ctc cgg cat cat tct gtc tgc cga ggg gct gat ctt gac caa caa cca cgt gat
 gly gly leu arg his his ser val cys arg gly ala asp leu asp gln gln pro arg asp
 1861/621
 cgc ggc ggc cgc caa gcc tcc cct ggg cag tcc gcc gcc gaa aac gac ggt a
 arg gly gly arg gln ala ser pro gly gln ser ala ala glu asn asp gly)

SEQ ID Nos 878-882 (continued 1)

FIGURE 49C (continued 1)

Coding sequence Rv0983 predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq60A:

1/1
 20 ID No 883 atg gcc aag ttg gcc cga gta gtg ggc cta gta cag gaa gag caa cct agc gac atg acg
 (Met ala lys leu ala arg val val gly leu val gln glu glu gln pro ser asp met thr
 20 ID No 884 61/21
 aat cac cca cgg tat tgc cca ccg ccg cag cag ccg gga acc cca ggt tat gct cag ggg
 asn his pro arg tyr ser pro pro pro gln gln pro gly thr pro gly tyr ala gln gly
 121/41
 cag cag caa acg tac agc cag cag ttc gac tgg cgt tac cca ccg tcc ccg ccc ccg cag
 gln gln gln thr tyr ser gln gln phe asp trp arg tyr pro pro ser pro pro pro gln
 181/61
 cca acc cag tac cgt caa ccc tac gag gcg ttg ggt ggt acc ccg ccg ggt ctg ata cct
 pro thr gln tyr arg gln pro tyr glu ala leu gly gly thr arg pro gly leu ile pro
 241/81
 ggc gtg att ccg acc atg acg ccc cct cct ggg atg gtt cgc caa cgc cct cgt gca ggc
 gly val ile pro thr met thr pro pro pro gly met val arg gln arg pro arg ala gly
 301/101
 atg ttg gcc atc ggc gcg gtg acg ata gcg gtg gtg tcc gcc ggc atc ggc ggc gcg gcc
 met leu ala ile gly ala val thr ile ala val val ser ala gly ile gly gly ala ala
 361/121
 gca tcc ctg gtc ggg ttc aac ccg gca ccc gcc ggc ccc agc ggc ggc cca gtg gct gcc
 ala ser leu val gly phe asn arg ala pro ala gly pro ser gly gly pro val ala ala
 421/141
 agc gcg gcg cca agc atc ccc gca gca aac atg ccg ccg ggg tgc gtc gaa cag gtg gcg
 ser ala ala pro ser ile pro ala ala asn met pro pro gly ser val glu gln val ala
 481/161
 gcc aag gtg gtg ccc agt gtc gtc atg ttg gaa acc gat ctg ggc cgc cag tgc gag gag
 ala lys val val pro ser val val met leu glu thr asp leu gly arg gln ser glu glu
 541/181
 ggc tcc ggc atc att ctg tct gcc gag ggg ctg atc ttg acc aac aac cac gtg atc gcg
 gly ser gly ile ile leu ser ala glu gly leu ile leu thr asn asn his val ile ala
 601/201
 gcg gcc gcc aag cct ccc ctg ggc agt ccg ccg ccg aaa acg acg gta acc ttc tct gac
 ala ala ala lys pro pro leu gly ser pro pro pro lys thr thr val thr phe ser asp
 661/221
 ggg ccg acc gca ccc ttc acg gtg gtg ggg gct gac ccc acc agt gat atc gcc gtc gtc
 gly arg thr ala pro phe thr val val gly ala asp pro thr ser asp ile ala val val
 721/241
 cgt gtt cag ggc gtc tcc ggg ctg acc ccg atc tcc ctg ggt tcc tcc tgc gac ctg agg
 arg val gln gly val ser gly leu thr pro ile ser leu gly ser ser ser asp leu arg
 781/261
 gtc ggt cag ccg gtg ctg gcg atc ggg tgc ccg ctg ggt ttg gag ggc acc gtg acc acg
 val gly gln pro val leu ala ile gly ser pro leu gly leu glu gly thr val thr thr

SEQ ID Nos. 883-884

FIGURE 49D

841/281	871/291
ggg atc gtc agc gct ctc aac cgt cca gtg	tcg acg acc ggc gag gcc ggc aac cag aac
gly ile val ser ala leu asn arg pro val	ser thr thr gly glu ala gly asn gln asn
901/301	931/311
acc gtg ctg gac gcc att cag acc gac gcc	gcg atc aac ccc ggt aac tcc ggg ggc gcg
thr val leu asp ala ile gln thr asp ala	ala ile asn pro gly asn ser gly gly ala
961/321	991/331
ctg gtg aac atg aac gct caa ctc gtc gga	gtc aac tcg gcc att gcc acg ctg ggc gcg
leu val asn met asn ala gln leu val gly	val asn ser ala ile ala thr leu gly ala
1021/341	1051/351
gac tca gcc gat gcg cag agc ggc tcg atc	ggg ctc ggt ttt gcg att cca gtc gac cag
asp ser ala asp ala gln ser gly ser ile	gly leu gly phe ala ile pro val asp gln
1081/361	1111/371
gcc aag cgc atc gcc gac gag ttg atc agc	acc ggc aag gcg tca cat gcc tcc ctg ggt
ala lys arg ile ala asp glu leu ile ser	thr gly lys ala ser his ala ser leu gly
1141/381	1171/391
gtg cag gtg acc aat gac aaa gac acc ctg	ggc gcc aag atc gtc gaa gta gtg gcc ggt
val gln val thr asn asp lys asp thr leu	gly ala lys ile val glu val val ala gly
1201/401	1231/411
ggt gct gcc gcg aac gct gga gtg ccg aag	ggc gtc gtt gtc acc aag gtc gac gac cgc
gly ala ala ala asn ala gly val pro lys	gly val val val thr lys val asp asp arg
1261/421	1291/431
ccg atc aac agc gcg gac gcg ttg gtt gcc	gcc gtg ccg tcc aaa gcg ccg ggc gcc acg
pro ile asn ser ala asp ala leu val ala	ala val arg ser lys ala pro gly ala thr
1321/441	1351/451
gtg gcg cta acc ttt cag gat ccc tcg ggc	ggt agc cgc aca gtg caa gtc acc ctc ggc
val ala leu thr phe gln asp pro ser gly	gly ser arg thr val gln val thr leu gly
1381/461	
aag gcg gag cag tga	
lys ala glu gln)OPA	

SEQ ID Nos 883-884(continued 1)

FIGURE 49D (continued 1)

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0983

1/1

31/11

SEQ ID NO. 885 tga gcc agc tcg acg cgt cgc acg ctg agc tgg tgg ttt ccg acc gcg gcc cgg gca ttc
 OPA/ala ser ser thr arg arg thr leu ser trp trp phe pro thr ala ala arg ala phe

61/21

91/31

ccg tgc agg agc gcc gtc tgg tgt ttg aac ggt ttt acc ggt cgg cat cgg cac ggg cgt
 pro cys arg ser ala val trp cys leu asn gly phe thr gly arg his arg his gly arg

121/41

151/51

tgc cgg gtt cgg gcc tcg ggt tgg cga tcg tca aac agg tgg tgc tca acc acg gcg gat
 cys arg val arg ala ser gly trp arg ser ser asn arg trp cys ser thr thr ala asp

181/61

211/71

tgc tgc gca tcg aag aca ccg acc cag gcg gcc agc ccc ctg gaa cgt cga ttt acg tgc
 cys cys ala ser lys thr pro thr gln ala ala ser pro leu glu arg arg phe thr cys

241/81

271/91

tgc tcc ccg gcc gtc gga tgc cga ttc cgc agc ttc ccg gtg cga cgg ctg gcg ctc gga
 cys ser pro ala val gly cys arg phe arg ser phe pro val arg arg leu ala leu gly

301/101

331/111

gca cgg aca tcg aga act ctc ggg gtt cgg cga acg tta tct cag tgg aat ctc agt cca
 ala arg thr ser arg thr leu gly val arg arg thr leu ser gln trp asn leu ser pro

361/121

391/131

cgc gcg caa cct agt tgt gca gtt act gtt gaa agc cac acc cat gcc agt cca cgc atg
 arg ala gln pro ser cys ala val thr val glu ser his thr his ala ser pro arg met

421/141

451/151

gcc aag ttg gcc cga gta gtg ggc cta gta cag gaa gag caa cct agc gac atg acg aat
 ala lys leu ala arg val val gly leu val gln glu glu gln pro ser asp met thr asn

481/161

511/171

cac cca cgg tat tcg cca ccg ccg cag cag ccg gga acc cca ggt tat gct cag ggg cag
 his pro arg tyr ser pro pro pro gln gln pro gly thr pro gly tyr ala gln gly gln

541/181

571/191

cag caa acg tac agc cag cag ttc gac tgg cgt tac cca ccg tcc ccg ccc ccg cag cca
 gln gln thr tyr ser gln gln phe asp trp arg tyr pro pro ser pro pro pro gln pro

601/201

631/211

acc cag tac cgt caa ccc tac gag gcg ttg ggt ggt acc cgg ccg ggt ctg ata cct ggc
 thr gln tyr arg gln pro tyr glu ala leu gly gly thr arg pro gly leu ile pro gly

661/221

691/231

gtg att ccg acc atg acg ccc cct cct ggg atg gtt cgc caa cgc cct cgt gca ggc atg
 val ile pro thr met thr pro pro pro gly met val arg gln arg pro arg ala gly met

721/241

751/251

ttg gcc atc ggc gcg gtg acg ata gcg gtg gtg tcc gcc ggc atc ggc ggc gcg gcc gca
 leu ala ile gly ala val thr ile ala val val ser ala gly ile gly gly ala ala ala

781/261

811/271

tcc ctg gtc ggg ttc aac ccg gca ccc gcc ggc ccc agc ggc ggc cca gtg gct gcc agc
 ser leu val gly phe asn arg ala pro ala gly pro ser gly gly pro val ala ala ser

841/281

871/291

gcg gcg cca agc atc ccc gca gca aac atg ccg ccg ggg tcg gtc gaa cag gtg gcg gcc
 ala ala pro ser ile pro ala ala asn met pro pro gly ser val glu gln val ala ala

SEQ ID NO. 885-886

FIGURE 49E

901/301	931/311
aag gtg gtg ccc agt gtc gtc atg ttg gaa	acc gat ctg ggc cgc cag tcg gag gag ggc
lys val val pro ser val val met leu glu	thr asp leu gly arg gln ser glu glu gly
961/321	991/331
tcc ggc atc att ctg tct gcc gag ggg ctg	atc ttg acc aac aac cac gtg atc gcg gcg
ser gly ile ile leu ser ala glu gly leu	ile leu thr asn asn his val ile ala ala
1021/341	1051/351
gcc gcc aag cct ccc ctg ggc agt ccg ccg	ccg aaa acg acg gta acc ttc tct gac ggc
ala ala lys pro pro leu gly ser pro pro	pro lys thr thr val thr phe ser asp gly
1081/361	1111/371
cgg acc gca ccc ttc acg gtg gtg ggg gct	gac ccc acc agt gat atc gcc gtc gtc cgt
arg thr ala pro phe thr val val gly ala	asp pro thr ser asp ile ala val val arg
1141/381	1171/391
ggt cag ggc gtc tcc ggg ctg acc ccg atc	tcc ctg ggt tcc tcc tcg gac ctg agg gtc
val gln gly val ser gly leu thr pro ile	ser leu gly ser ser ser asp leu arg val
1201/401	1231/411
ggt cag ccg gtg ctg gcg atc ggg tcg ccg	ctc ggt ttg gag ggc acc gtg acc acg ggc
gly gln pro val leu ala ile gly ser pro	leu gly leu glu gly thr val thr thr gly
1261/421	1291/431
atc gtc agc gct ctg aac cgt cca gtg tcg	acg acc ggc gag gcc ggc aac cag aac acc
ile val ser ala leu asn arg pro val ser	thr thr gly glu ala gly asn gln asn thr
1321/441	1351/451
gtg ctg gac gcc att cag acc gac gcc gcg	atc aac ccc ggt aac tcc ggg ggc gcg ctg
val leu asp ala ile gln thr asp ala ala	ile asn pro gly asn ser gly gly ala leu
1381/461	1411/471
gtg aac atg aac gct caa ctg gtc gga gtc	aac tcg gcc att gcc acg ctg ggc gcg gac
val asn met asn ala gln leu val gly val	asn ser ala ile ala thr leu gly ala asp
1441/481	1471/491
tca gcc gat gcg cag agc ggc tcg atc ggt	ctc ggt ttt gcg att cca gtc gac cag gcc
ser ala asp ala gln ser gly ser ile gly	leu gly phe ala ile pro val asp gln ala
1501/501	1531/511
aag cgc atc gcc gac gag ttg atc agc acc	ggc aag gcg tca cat gcc tcc ctg ggt gtg
lys arg ile ala asp glu leu ile ser thr	gly lys ala ser his ala ser leu gly val
1561/521	1591/531
cag gtg acc aat gac aaa gac acc ctg ggc	gcc aag atc gtc gaa gta gtg gcc ggt ggt
gln val thr asn asp lys asp thr leu gly	ala lys ile val glu val val ala gly gly
1621/541	1651/551
gct gcc gcg aac gct gga gtg ccg aag ggc	gtc gtt gtc acc aag gtc gac gac cgc ccg
ala ala ala asn ala gly val pro lys gly	val val val thr lys val asp asp arg pro
1681/561	1711/571
atc aac agc gcg gac gcg ttg gtt gcc gcc	gtg cgg tcc aaa gcg ccg ggc gcc acg gtg
ile asn ser ala asp ala leu val ala ala	val arg ser lys ala pro gly ala thr val
1741/581	1771/591
gcg cta acc ttt cag gat ccc tcg ggc ggt	agc cgc aca gtg caa gtc acc ctg ggc aag
ala leu thr phe gln asp pro ser gly gly	ser arg thr val gln val thr leu gly lys
1801/601	
gcg gag cag tga	
ala glu gln)OPA	

SEQ ID Nos. 885-886 (continued 1)

FIGURE 49E (continued 1)

Fragment amplified by PCR based on the sequence similarities with a serine protease of the E.coli HtrA family (creation of an SnaBI site at the 3' end) and subcloned into the vector pJVEDa:

1/1
 gat ccg gcg ggg cgg gtg tcg gcg cag gcg tgg ctg gcg gtc acg gcg gtg cgg gcg gtg
 (asp pro ala gly arg val ser ala gln ala trp leu ala val thr ala val arg ala val
 61/21
 ccg ccg ggc tgt ggg gcg ccg gcg gcg gcg gtg gca atg gcg gga acg gcg ccg atg cca
 pro pro gly cys gly ala pro ala ala ala val ala met ala gly thr ala pro met pro
 121/41
 aca tcg tca gcg gtg gag acg gtg gcc tcg gcg gtg ccg gtg gcg gtg gcg gat ggc tct
 thr ser ser ala val glu thr val ala ser ala val pro val ala val ala asp gly ser
 181/61
 acg gcg acg gcg ggg ccg gcg gac acg gcg gac aag gcg caa tcg gcc tcg gcg gcg gcg
 thr ala thr ala gly pro ala asp thr ala asp lys ala gln ser ala ser ala ala ala
 241/81
 ccg gcg gcg acg ggg gcc agg gcg gcg ccg gcc gcg gac tgt ggg gta ctg gcg gcg ccg
 pro ala ala thr gly ala arg ala ala pro ala ala asp cys gly val leu ala ala pro
 301/101
 gcg gac acg gcg ggc aag gcg gtg gta ccg ggg gcc cac cgc tgc ccg gtc agg cag gca
 ala asp thr ala gly lys ala val val pro gly ala his arg cys pro val arg gln ala
 361/121
 tgg gcg ccg ccg gtg gcg ccg gtg ggc tga tcg gca acg gcg ggg ccg gcg gcg acg gcg
 trp ala pro arg val ala pro val gly) OPA (ser ala thr ala gly pro ala ala thr ala
 421/141
 gtg tcg gcg cgt ccg gcg ggg tcg ccg gag tag gcg gtg ccg gcg gga acg cca tgc tga
 val ser ala arg pro ala gly ser pro glu) AMB (ala val pro ala gly thr pro cys) OPA
 481/161
 tcg ggc acg gcg gcg ccg gcg gcg ccg gcg gag aca gca gtt tcg cta atg gcg ccg ccg
 (ser gly thr ala ala pro ala ala pro ala glu thr ala val ser leu met ala arg pro
 541/181
 gcg gcg ccg gcg gtg ccg gag ggc acc tct tcg gca atg gcg ggt ccg gcg gcc acg gcg
 ala ala arg ala val pro glu gly thr ser ser ala met ala gly pro ala ala thr ala
 601/201
 gag ccg tca ccg ccg gca aca ccg gta tcg gtg gcg ccg gcg gcg tcg gtg ggg acg cca
 glu pro ser arg pro ala thr pro val ser val ala pro ala ala ser val gly thr pro
 661/221
 ggc tga tcg gcc acg gtg gcg ccg gcg gtg ccg gcg ggg acc gcg ccg gag cct tgg ttg
 gly) OPA (ser ala thr val ala pro ala val pro ala gly thr ala pro glu pro trp leu
 721/241
 gcc gtg acg gcg ggc ccg gtg gga acg ggg gcg ctg gcg gcc agc tat acg gca acg gcg
 ala val thr ala gly pro val gly thr gly ala leu ala ala ser tyr thr ala thr ala
 781/261
 gcg acg gcg ccc ccg gca ccg gcg gaa cac tgc agg ccg ccg tga gcg gat tgg tga ccg
 ala thr ala pro pro ala pro ala glu his cys arg arg arg) OPA ala asp trp OPA (arg
 841/281
 ctt tgt tcg gtg cac ccg gcc aac ccg gcg aca ccg gcc aac ccg gct agc ccc gat caa
 leu cys ser val his pro ala asn pro ala thr pro ala asn pro ala ser pro asp gln
 901/301
 cga ggg ttt ccg tgc ccg tcc ggg gca tgg cca tcc gct gag ctg gcg atc tgg act acg
 arg gly phe arg cys arg ser gly ala trp pro ser ala glu leu ala ile trp thr thr
 961/321
 ttg gtg tag aaa aat cct gcc gcc ccg acc ctt aag gct ggg aca att tct gat agc tac
 leu val) AMB (lys asn pro ala ala arg thr leu lys ala gly thr ile ser asp ser tyr
 1021/341
 ccc gac aca gga ggt tac ggg atg agc aat tcg cgc cgc cgc tca ctc agg tgg tca tgg
 pro asp thr gly gly tyr gly met ser asn ser arg arg arg ser leu arg trp ser trp
 1081/361
 ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc ctg gcc acg gcg ccg gcc cag gcg gcc
 leu leu ser val leu ala ala val gly leu gly leu ala thr ala pro ala gln ala ala
 1141/381
 ccg ccg gcc ttg tcg cag gac ccg tt
 pro pro ala leu ser gln asp arg)

SEQ ID No. 887
 SEQ ID No. 888
 SEQ ID No. 889
 SEQ ID No. 890
 SEQ ID No. 891
 SEQ ID No. 892
 SEQ ID No. 893
 SEQ ID No. 894

1/1
 atc cgg cgg ggc ggg tgt cgg cgc agg cgt ggc tgg cgg tca cgg cgg tgc ggg cgg tgc
 ile arg arg gly gly cys arg arg arg arg gly trp arg ser arg arg cys gly arg cys
 61/21
 cgc cgg gct gtg ggg cgc cgg cgg cgg cgg tgg caa tgg cgg gaa cgg cgc cga tgc caa
 arg arg ala val gly arg arg arg arg trp gln trp arg glu arg arg arg cys gln
 121/41
 cat cgt cag cgg tgg aga cgg tgg cct cgg cgg tgc cgg tgg cgg tgg cgg atg gct cta
 his arg gln arg trp arg arg trp pro arg arg cys arg trp arg trp arg met ala leu
 181/61
 cgg cga cgg cgg ggc cgg cgg aca cgg cgg aca agg cgc aat cgg cct cgg cgg cgg cgc
 arg arg arg arg gly arg arg thr arg arg thr arg arg asn arg pro arg arg arg arg
 241/81
 cgg cgg cga cgg ggg cca ggg cgg cgc cgg ccg cgg act gtg ggg tac tgg cgg cgc cgg
 arg arg arg arg gly pro gly arg arg arg pro arg thr val gly tyr trp arg arg arg
 301/101
 cgg aca cgg cgg gca agg cgg tgg tac cgg ggg ccc acc gct gcc cgg tca ggc agg cat
 arg thr arg arg ala arg arg trp tyr arg gly pro thr ala ala arg ser gly arg his
 361/121
 ggg cgc cgc ggg tgg cgc cgg tgg gct gat cgg caa cgg cgg ggc cgg cgg cga cgg cgg
 gly arg arg gly trp arg arg trp ala asp arg gln arg arg gly arg arg arg arg
 421/141
 tgt cgg cgc gtc cgg cgg ggt cgc cgg agt agg cgg tgc cgg cgg gaa cgc cat gct gat
 cys arg arg val arg arg gly arg arg ser arg arg cys arg arg glu arg his ala asp
 481/161
 cgg gca cgg cgg cgc cgg cgg cgc cgg cgg aga cag cag ttt cgc taa tgg cgc ggc cgg
 arg ala arg arg arg arg arg arg arg arg arg gln gln phe arg) OCH(trp arg gly arg
 541/181
 cgg cgc ggg cgg tgc cgg agg gca cct ctt cgg caa tgg cgg gtc cgg cgg cca cgg cgg
 arg arg gly arg cys arg arg ala pro leu arg gln trp arg val arg arg pro arg arg
 601/201
 agc cgt cac ggc cgg caa cac cgg tat cgg tgg cgc cgg cgg cgt cgg tgg gga cgc cag
 ser arg his gly arg gln his arg tyr arg trp arg arg arg arg arg trp gly arg gln
 661/221
 gct gat cgg cca cgg tgg cgc cgg cgg tgc cgg cgg gga ccg cgc cgg agc ctt ggt tgg
 ala asp arg pro arg trp arg arg arg cys arg arg gly pro arg arg ser leu gly trp
 721/241
 ccg tga cgg cgg gcc cgg tgg gaa cgg ggg cgc tgg cgg cca gct ata cgg caa cgg cgg
 pro) OPA(arg arg ala arg trp glu arg gly arg trp arg pro ala ile arg gln arg arg
 781/261
 cga cgg cgc ccc cgg cac cgg cgg aac act gca ggc ggc ggt gag cgg att ggt gac ggc
 arg arg arg pro arg his arg arg asn thr ala gly gly gly glu arg ile gly asp gly
 841/281
 ttt gtt cgg tgc acc cgg cca acc cgg cga cac cgg cca acc cgg cta gcc ccg atc aac
 phe val arg cys thr arg pro thr arg arg his arg pro thr arg leu ala pro ile asn
 901/301
 gag ggt ttc ggt gcc ggt ccg ggg cat ggc cat ccg ctg agc tgg cga tct gga cta cgt
 glu gly phe gly ala gly pro gly his gly his pro leu ser trp arg ser gly leu arg
 961/321
 tgg tgt aga aaa atc ctg ccg ccc gga ccc tta agg ctg gga caa ttt ctg ata gct acc
 trp cys arg lys ile leu pro pro gly pro leu arg leu gly gln phe leu ile ala thr
 1021/341
 ccg aca cag gag gtt acg gga tga gca att cgc gcc gcc gct cac tca ggt ggt cat ggt
 pro thr gln glu val thr gly) OPA(ala ile arg ala ala ala his ser gly gly his gly
 1081/361
 tgc tga gcg tgc tgg ctg ccg tgc ggc tgg gcc tgg cca cgg cgc cgg ccc agg cgg ccc
 cys) OPA(ala cys trp leu pro ser gly trp ala trp pro arg arg arg pro arg arg pro
 1141/381
 cgc cgg cct tgt cgc agg acc ggt t
 arg arg pro cys arg arg thr gly)

1/1
 SEQ ID No. 901
 SEQ ID No. 902
 61/21
 gcc ggg ctg tgg ggc gcc ggc ggc ggc ggt ggc aat ggc ggg aac ggc gcc gat gcc aac
 ala gly leu trp gly ala gly gly gly gly gly gly asn gly gly asn gly ala asp ala asn
 121/41
 atc gtc agc ggt gga gac ggt ggc ctc ggc ggt gcc ggt ggc ggt ggc gga tgg ctc tac
 ile val ser gly gly asp gly gly leu gly gly ala gly gly gly gly gly gly trp leu tyr
 181/61
 ggc gac ggc ggg gcc ggc gga cac ggc gga caa ggc gca atc ggc ctc ggc ggc ggc gcc
 gly asp gly gly ala gly gly his gly gly gln gly ala ile gly leu gly gly gly ala
 241/81
 ggc ggc gac ggg ggc cag ggc ggc gcc ggc cgc gga ctg tgg ggt act ggc ggc gcc ggc
 gly gly asp gly gly gln gly gly ala gly arg gly leu trp gly thr gly gly ala gly
 301/101
 gga cac ggc ggg caa ggc ggt ggt acc ggc ggc cca ccg ctg ccc ggt cag gca ggc atg
 gly his gly gly gln gly gly gly thr gly gly pro pro leu pro gly gln ala gly met
 361/121
 ggc gcc gcg ggt ggc gcc ggt ggg ctg atc ggc aac ggc ggg gcc ggc ggc gac ggc ggt
 gly ala ala gly gly ala gly gly leu ile gly asn gly gly ala gly gly asp gly gly
 421/141
 gtc ggc gcg tcc ggc ggg gtc gcc gga gta ggc ggt gcc ggc ggg aac gcc atg ctg atc
 val gly ala ser gly gly val ala gly val gly gly ala gly gly asn ala met leu ile
 481/161
 ggg cac ggc ggc gcc ggc ggc gcc ggc gga gac agc agt ttc gct aat ggc gcg gcc ggc
 gly his gly gly ala gly gly ala gly gly asp ser phe ala asn gly ala ala gly
 541/181
 ggc gcg ggc ggt gcc gga ggg cac ctc ttc ggc aat ggc ggg tcc ggc ggc cac ggc gga
 gly ala gly gly ala gly gly his leu phe gly asn gly gly ser gly gly his gly gly
 601/201
 gcc gtc acg gcc ggc aac acc ggt atc ggt ggc gcc ggc ggc gtc ggt ggg gac gcc agg
 ala val thr ala gly asn thr gly ile gly gly ala gly gly val gly gly asp ala arg
 661/221
 ctg atc ggc cac ggt ggc gcc ggc ggt gcc ggc ggg gac cgc gcc gga gcc ttg gtt ggc
 leu ile gly his gly gly ala gly gly ala gly gly asp arg ala gly ala leu val gly
 721/241
 cgt gac ggc ggg ccc ggt ggg aac ggg ggc gct ggc ggc cag cta tac ggc aac ggc ggc
 arg asp gly gly pro gly gly asn gly gly ala gly gly gln leu tyr gly asn gly gly
 781/261
 gac ggc gcc ccc ggc acc ggc gga aca ctg cag gcg gcg gtg agc gga ttg gtg acg gct
 asp gly ala pro gly thr gly gly thr leu gln ala ala val ser gly leu val thr ala
 841/281
 ttg ttc ggt gca ccc ggc caa ccc ggc gac acc ggc caa ccc ggc tag ccc cga tca acg
 leu phe gly ala pro gly gln pro gly asp thr gly gln pro gly) AMB (pro arg ser thr
 901/301
 agg gtt tcg gtg ccg gtc cgg ggc atg gcc atc cgc tga gct ggc gat ctg gac tac gtt
 arg val ser val pro val arg gly met ala ile arg) OPA (ala gly asp leu asp tyr val
 961/321
 ggt gta gaa aaa tcc tgc cgc ccg gac cct taa ggc tgg gac aat ttc tga tag cta ccc
 gly val glu lys ser cys arg pro asp pro) OCH (gly trp asp asn phe) OPA AMB (leu pro
 1021/341
 cga cac agg agg tta cgg gat gag caa ttc gcg ccg ccg ctc act cag gtg gtc atg gtt
 arg his arg arg leu arg asp glu gln phe ala pro pro leu thr gln val val met val
 1081/361
 gct gag cgt gct ggc tgc cgt cgg gct ggg cct ggc cac ggc gcc ggc cca ggc ggc ccc
 ala glu arg ala gly cys arg arg ala gly pro gly his gly ala gly pro gly gly pro
 1141/381
 gcc ggc ctt gtc gca gga ccg gtt
 ala gly leu val ala gly pro val)

179/185

Coding sequence Rv0125 predicted by Cole et al., 1998 (Nature 393:537-544) and containing seq50A:

1/1	31/11
atg agc aat tcg cgc cgc cgc tca ctc agg	tgg tca tgg ttg ctg agc gtg ctg gct gcc
Met ser asn ser arg arg arg ser leu arg	trp ser trp leu leu ser val leu ala ala
61/21	91/31
gtc ggg ctg ggc ctg gcc acg gcg ccg gcc	cag gcg gcc ccg ccg gcc ttg tcg cag gac
val gly leu gly leu ala thr ala pro ala	gln ala ala pro pro ala leu ser gln asp
121/41	151/51
cgg ttc gcc gac ttc ccc gcg ctg ccc ctc	gac ccg tcc gcg atg gtc gcc caa gtg ggg
arg phe ala asp phe pro ala leu pro leu	asp pro ser ala met val ala gln val gly
181/61	211/71
cca cag gtg gtc aac atc aac acc aaa ctg	ggc tac aac aac gcc gtg ggc gcc ggg acc
pro gln val val asn ile asn thr lys leu	gly tyr asn asn ala val gly ala gly thr
241/81	271/91
ggc atc gtc atc gat ccc aac ggt gtc gtg	ctg acc aac aac cac gtg atc gcg ggc gcc
gly ile val ile asp pro asn gly val val	leu thr asn asn his val ile ala gly ala
301/101	331/111
acc gac atc aat gcg ttc agc gtc ggc tcc	ggc caa acc tac ggc gtc gat gtg gtc ggg
thr asp ile asn ala phe ser val gly ser	gly gln thr tyr gly val asp val val gly
361/121	391/131
tat gac cgc acc cag gat gtc gcg gtg ctg	cag ctg cgc ggt gcc ggt ggc ctg ccg tcg
tyr asp arg thr gln asp val ala val leu	gln leu arg gly ala gly gly leu pro ser
421/141	451/151
gcg gcg atc ggt ggc ggc gtc gcg gtt ggt	gag ccc gtc gtc gcg atg ggc aac agc ggt
ala ala ile gly gly gly val ala val gly	glu pro val val ala met gly asn ser gly
481/161	511/171
ggg cag ggc gga acg ccc cgt gcg gtg cct	ggc agg gtg gtc gcg ctc ggc caa acc gtg
gly gln gly gly thr pro arg ala val pro	gly arg val val ala leu gly gln thr val
541/181	571/191
cag gcg tcg gat tcg ctg acc ggt gcc gaa	gag aca ttg aac ggg ttg atc cag ttc gat
gln ala ser asp ser leu thr gly ala glu	glu thr leu asn gly leu ile gln phe asp
601/201	631/211
gcc gcg atc cag ccc ggt gat tcg ggc ggg	ccc gtc gtc aac ggc cta gga cag gtg gtc
ala ala ile gln pro gly asp ser gly gly	pro val val asn gly leu gly gln val val
661/221	691/231
ggt atg aac acg gcc gcg tcc gat aac ttc	cag ctg tcc cag ggt ggg cag gga ttc gcc
gly met asn thr ala ala ser asp asn phe	gln leu ser gln gly gly gln gly phe ala
721/241	751/251
att ccg atc ggg cag gcg atg gcg atc gcg	ggc cag atc cga tcg ggt ggg ggg tca ccc
ile pro ile gly gln ala met ala ile ala	gly gln ile arg ser gly gly gly ser pro
781/261	811/271
acc gtt cat atc ggg cct acc gcc ttc ctc	ggc ttg ggt gtt gtc gac aac aac ggc aac
thr val his ile gly pro thr ala phe leu	gly leu gly val val asp asn asn gly asn
841/281	871/291
ggc gca cga gtc caa cgc gtg gtc ggg agc	gct ccg gcg gca agt ctc ggc atc tcc acc
gly ala arg val gln arg val val gly ser	ala pro ala ala ser leu gly ile ser thr
901/301	931/311
ggc gac gtg atc acc geg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg gac	gly asp val ile thr ala val asp gly ala pro ile asn ser ala thr ala met ala asp
961/321	991/331
gcg ctt aac ggg cat cat ccc ggt gac gtc	atc tcg gtg acc tgg caa acc aag tcg ggc
ala leu asn gly his his pro gly asp val	ile ser val thr trp gln thr lys ser gly
1021/341	1051/351
ggc acg cgt aca ggg aac gtg aca ttg gcc	gag gga ccc ccg gcc tga
gly thr arg thr gly asn val thr leu ala	glu gly pro pro ala) OPA

SEQ ID Nos. 907 - 908

FIGURE 50D

ORF according to Cole et al., 1998 (Nature 393:537-544) and containing Rv0125:

1/1
tag aaa aat cct gcc gcc cgg acc ctt aag gct ggg aca att tct gat agc tac ccc gac
AMB (lys asn pro ala ala arg thr leu lys ala gly thr ile ser asp ser tyr pro asp
61/21
aca gga ggt tac ggg atg agc aat tcg cgc cgc cgc tca ctc agg tgg tca tgg ttg ctg
thr gly gly tyr gly met ser asn ser arg arg arg ser leu arg trp ser trp leu leu
121/41
agc gtg ctg gct gcc gtc ggg ctg ggc ctg gcc acg ggc ccg gcc cag ggc gcc ccg ccg
ser val leu ala ala val gly leu gly leu ala thr ala pro ala gln ala ala pro pro
181/61
gcc ttg tcg cag gac cgg ttc gcc gac ttc ccc ggc ctg ccc ctc gac ccg tcc ggc atg
ala leu ser gln asp arg phe ala asp phe pro ala leu pro leu asp pro ser ala met
241/81
gtc gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac gcc
val ala gln val gly pro gln val val asn ile asn thr lys leu gly tyr asn asn ala
301/101
gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac
val gly ala gly thr gly ile val ile asp pro asn gly val val leu thr asn asn his
361/121
gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc caa acc tac ggc
val ile ala gly ala thr asp ile asn ala phe ser val gly ser gly gln thr tyr gly
421/141
gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc
val asp val val gly tyr asp arg thr gln asp val ala val leu gln leu arg gly ala
481/161
ggt ggc ctg ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg
gly gly leu pro ser ala ala ile gly gly gly val ala val gly glu pro val val ala
541/181
atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg
met gly asn ser gly gly gln gly gly thr pro arg ala val pro gly arg val val ala
601/201
ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag aca ttg aac ggg
leu gly gln thr val gln ala ser asp ser leu thr gly ala glu glu thr leu asn gly
661/221
ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc
leu ile gln phe asp ala ala ile gln pro gly asp ser gly gly pro val val asn gly
721/241
cta gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt
leu gly gln val val gly met asn thr ala ala ser asp asn phe gln leu ser gln gly
781/261
ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg
gly gln gly phe ala ile pro ile gly gln ala met ala ile ala gly gln ile arg ser
841/281
ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc
gly gly gly ser pro thr val his ile gly pro thr ala phe leu gly leu gly val val
901/301
gac aac aac ggc aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt
asp asn asn gly asn gly ala arg val gln arg val val gly ser ala pro ala ala ser
961/321
ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc
leu gly ile ser thr gly asp val ile thr ala val asp gly ala pro ile asn ser ala
1021/341
acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg-gtg-acc tgg
thr ala met ala asp ala leu asn gly his his pro gly asp val ile ser val thr trp
1081/361
caa acc aag tcg ggc ggc acg cgt aca ggg aac ggt aca ttg gcc gag gga ccc ccg gcc
gln thr lys ser gly gly thr arg thr gly asn val thr leu ala glu gly pro pro ala)
1141/381
tga
OPA

SEQ ID Nos. 909-910

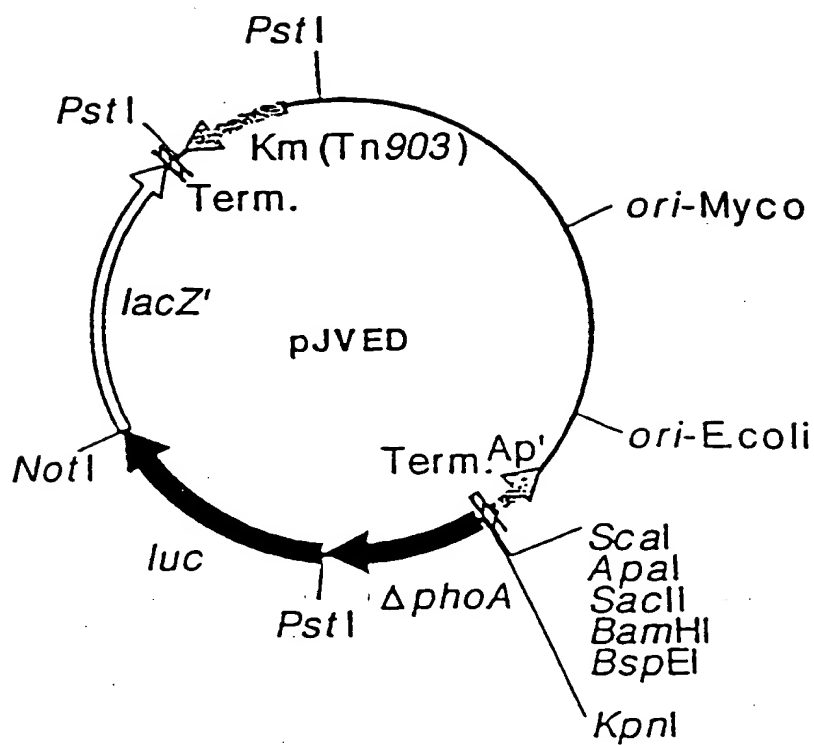


FIGURE 51A

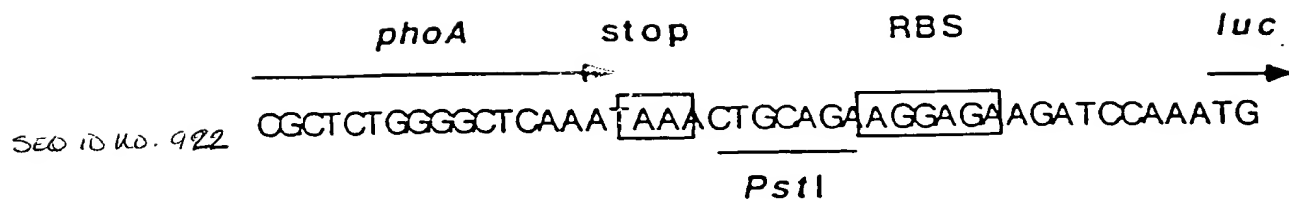


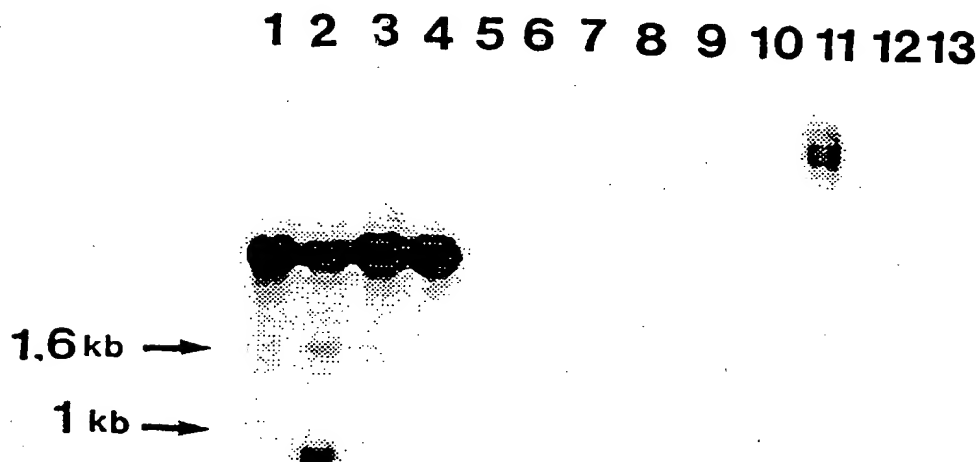
FIGURE 51



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Experiment of molecular hybridization of a specific to DP428 on the genomic DNA of various mycobacterial species



1: *M. tuberculosis* 2: *M. bovis* 3: BCG 4: *M. africanum* 5: cancelled 6: *M. fortuitum* 7: *M. simiae* 8: *M. avium* 9: *M. chelonae* 10: *M. flavescens* 11: *M. gordonae* 12: *M. marinum* 13: *M. kansasii*

FIGURE 52

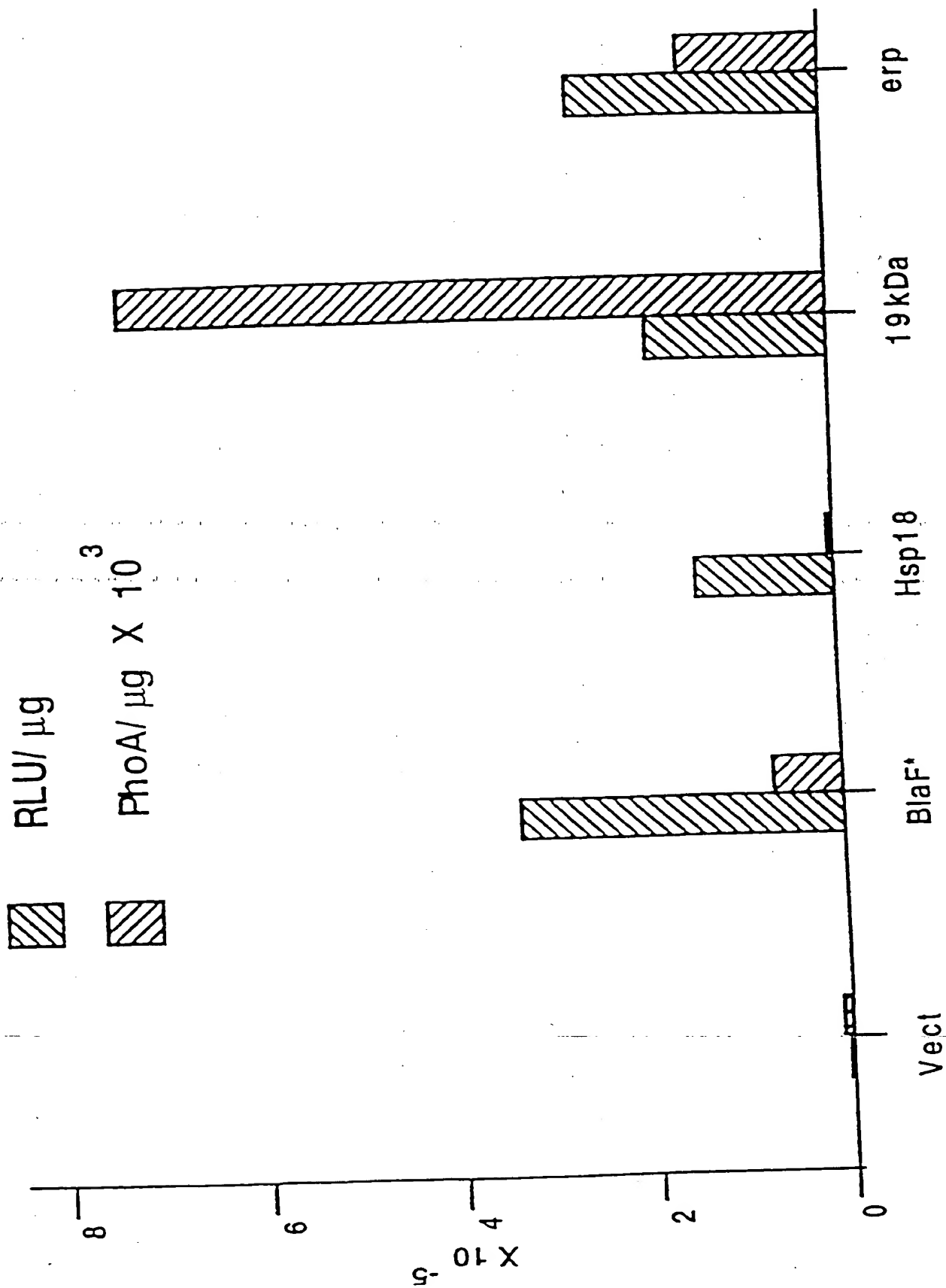


FIGURE 53

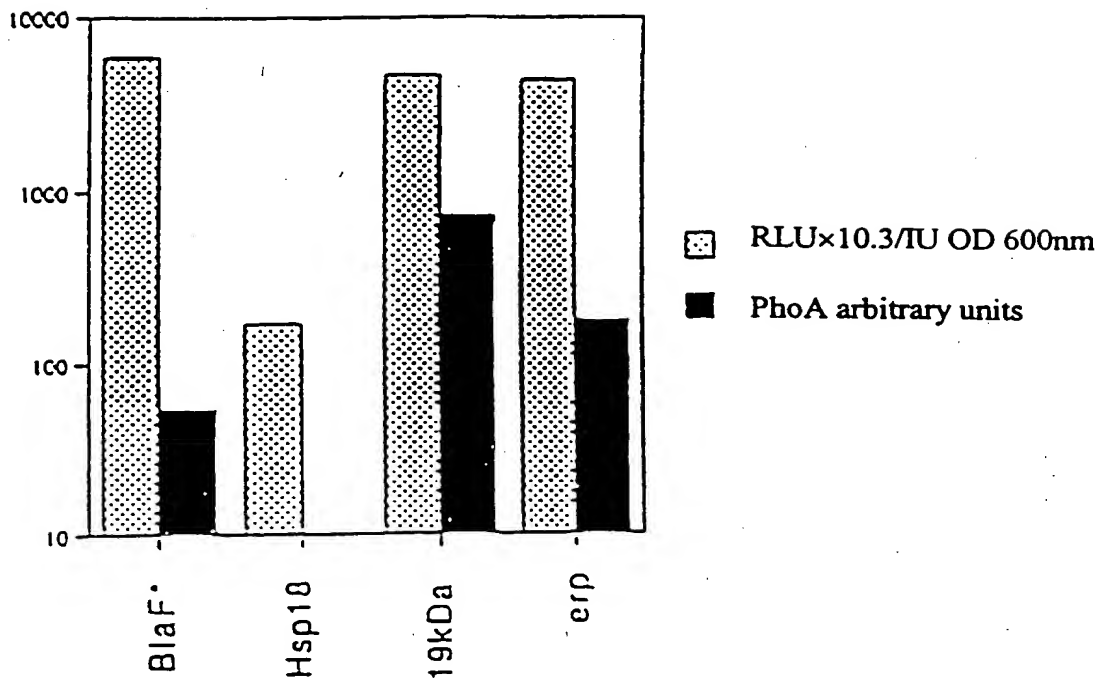


FIGURE 54

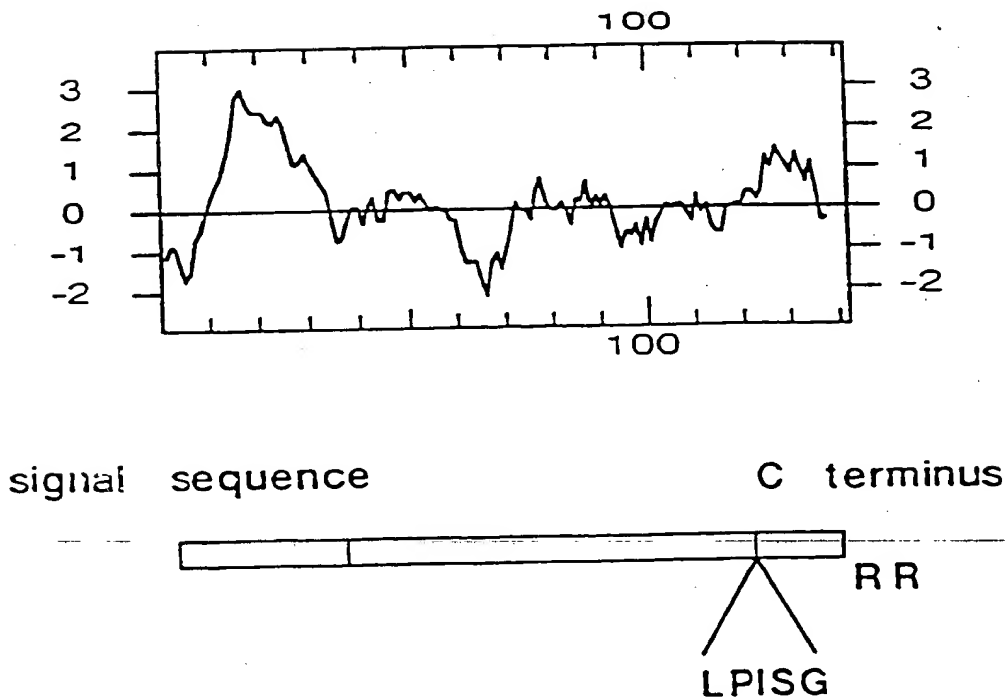


FIGURE 55



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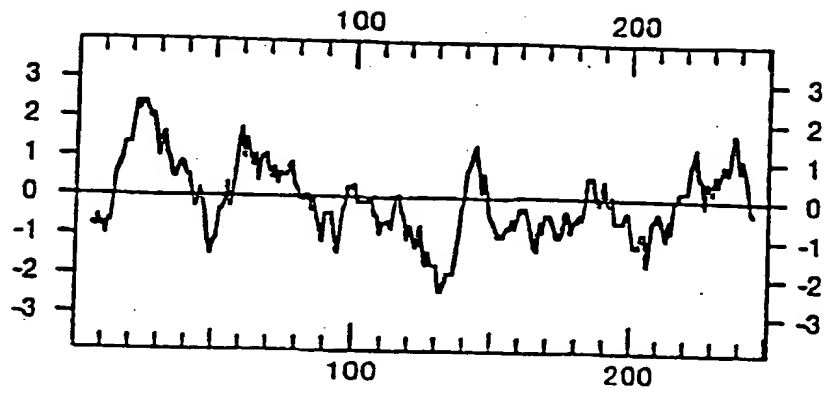


FIGURE 56

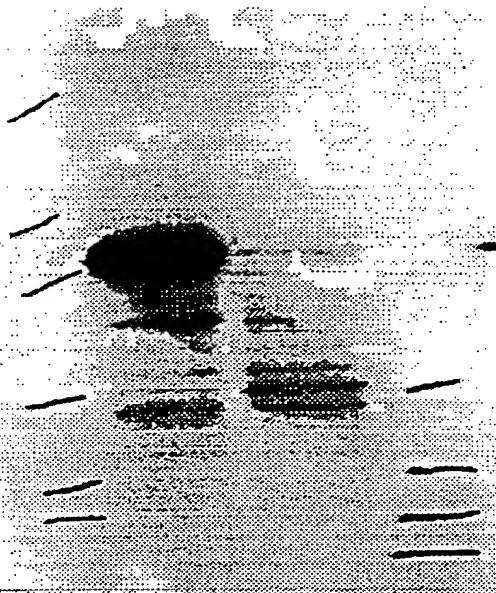


FIGURE 57A

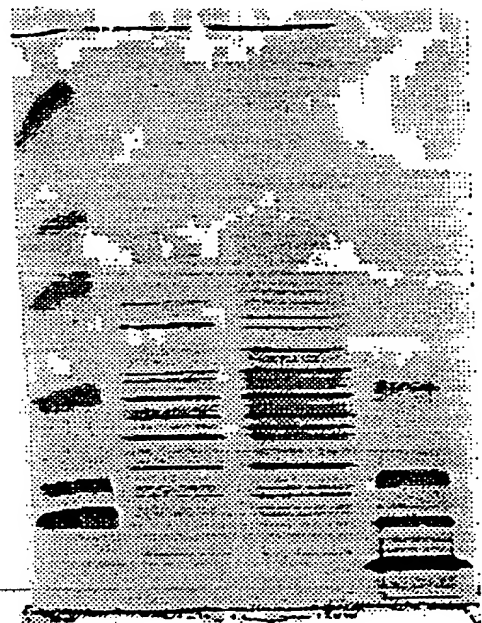


FIGURE 57B